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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2004, 11:03:00 ; Search time 647 Seconds (without alignments)

Title: US-09-837-602-2

Perfect score: 4033.697 Million cell updates/sec

Sequence: 1 MKKLPPAAGPAGGEPYRLT.....KEESLADDLFRYNPPYKRRR 754

Scoring table: BL0SUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0†

Maximum Match 100‡

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USP10_spool/US09837602/runat_06012004_104000_12487/app_query.fasta_1.903
-DB=Published_Application_NA -QFTX=rnbp -MINMATCH=0..1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=b1blob62
-TRANS:human40_d1 -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFILE=pto -NORM=ext -HEAPSIZEx=500 -MINLEN=0
-MAXLEN=200000000 -MODB=LOCAL -OUTFILE=pto -NORM=ext -HEAPSIZEx=500 -MINLEN=0
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEALIGN -NEGSCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=1:120 -WARN TIMEOUT=3:30 -THREADES=1 -XGAPOP=10 -XGAPEXT=0..5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0..5 -DELOP=6 -DELEXT=7

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Database :

Published Applications NA: *

- /cgn2_6/podata/1/pubnra/us07_pubcomb.seq*
- /cgn2_6/podata/1/pubnra/pct_new_pub.seq*
- /cgn2_6/podata/1/pubnra/us05_new_pub.seq*
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- /cgn2_6/podata/1/pubnra/us10c_new_pub.seq*
- /cgn2_6/podata/1/pubnra/us60_pubcomb.seq*

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ALIGNMENTS

RESULT 1
US-09-917-8004-803/c

Sequence 803, Application US/09917800A

Patent No. US20020119462A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

INVENTOR: Portier, Mark

APPLICANT: Johnson, Cory

APPLICANT: Castle, Arthur

APPLICANT: Elashoff, Michael

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5018-US

CURRENT APPLICATION NUMBER: US/09/917,800A

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/222,880

PRIOR FILING DATE: 2000-11-02

PRIOR APPLICATION NUMBER: US 60/290,029

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/290,645

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: US 60/292,336

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06 US 60/297,457
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13 US 60/298,884
 PRIOR APPLICATION NUMBER: US 60/298,884
 PRIOR FILING DATE: 2001-06-19 US 60/303,459
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09 US-09-923-876-5167
 NUMBER OF SEQ ID NOS: 1740 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 803 LENGTH: 475
 TYPE: DNA ORGANISM: Rattus norvegicus
 FEATURE: OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1137049
 US-09-917-800A-803

Alignment Scores:
 Pred. No.: 1.46e-32 Length: 475
 Score: 416.50 Matches: 82
 Percent Similarity: 83.64% Conservative: 10
 Best Local Similarity: 74.55% Mismatches: 17
 Query Match: 10.68% Indels: 1
 DB: 10 Gaps: 1

US-09-837-602-2 (1-754) x US-09-923-876-5167 (1-272)

Alignment Scores:
 Pred. No.: 1.47e-30 Length: 272
 Score: 393.00 Matches: 77
 Percent Similarity: 96.30% Conservative: 1
 Best Local Similarity: 95.06% Mismatches: 3
 Query Match: 10.08% Indels: 0
 DB: 9 CTTTTAGACAAACAAACACCTGTCAACNCTCATGTGAAATAAGAGGAGCATTTA 122

US-09-837-602-2 (1-754) x US-09-917-800A-803 (1-475)

Qy 644 GlnAspAspSerGluNetLeuProLysLeuLeuThrGluPheArgserieuval 663
 Db 474 CAAAGATTGGCACGGCTTCAAGAAACTGCTGCTGACTGAAATTAGGTCACTGGTT 415

Qy 664 IleLysSerThrSerArgAsnProSerLysLeuAspAspTyrGlyGlnLeuLys 683
 Db 414 GTCCATATAACTCTCCAGAAATCTGCCACTAAAT--GGTGTGGTGACTGAG 358

Qy 684 AsnPhenylslyPhenylslyValThrThrProGlyAlaGlyLysLeuProHisIle 703
 Db 357 ATTCAAGAATTCAAGAACGCTAGTGTCTGGAGCAAGACCTTACACATTATT 298

Qy 704 GlyGlySerAspLeuAlaHisIleAlaArgLysAsnThrGluLeuGluLysIle 723
 Db 297 GGAGGTCAAGATTATAAGTCACCATGTCGAAGAAATTCTGAAATTAGAGTGTTG 238

Qy 724 ArgGlnGlnMetGluValGlnGlnLysIleAlaLysGluGluSerLeuAlaAspAspIle 743
 Db 237 AAACATGAATGGAGTCAAGAAACACAGCGAAAGACTCTCTGCTGATGATCTG 178

Qy 744 PheArgTrpAsnProTyrLeuLeuLysArg 753
 Db 177 TTATGATATACTCTAATGTAATAAGAAGA 148

RESULT 2 US-09-923-876-5167
 Sequence 5167, Application US/09923876
 Patent No. US2002013958A1

GENERAL INFORMATION:
 APPLICANT: Laljudi, Raghunath V.
 APPLICANT: Kamigaki, Laura Y. (Ito)
 APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876
 CURRENT FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: 09/298,329
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 60/085,331
 PRIOR FILING DATE: 1998-05-05
 NUMBER OF SEQ ID NOS: 6332
 SOFTWARE: PERL Program
 SEQ ID NO: 5167 LENGTH: 272
 OTHER INFORMATION: Incyte ID No. US20030237110A9 700456477H1
 NAME/KEY: unsure
 LOCATION: 91, 242, 246, 256, 258, 260, 267, 270
 OTHER INFORMATION: a, t, c, g, or other
 US-09-923-876-5167

Alignment Scores:
 Pred. No.: 1.47e-30 Length: 272
 Score: 393.00 Matches: 77

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Percent Similarity: 96.30% Conservative: 1
 Best Local Similarity: 95.06% Mismatches: 3
 Query Match: 10.08% Indels: 0
 DB: 12 Gaps: 0

US-09-837-602-2 (1-754) x US-09-923-876-5167 (1-272)

Qy 469 AspGluGluAsnGlnGluMetSerSerCysIleSerAlaArgIleGluThrSerCysSer 488
 Db 3 GATGAGAAATCAAAATCTCTCATGCAAACTCGCAATG 62

Qy 489 LeuLeuGluGlnThrIleProAlaThrProLeuLeuLeuGluGlnIleLeu 508
 Db 63 CTTTTAGAAACAACACACACCTGCTACACNTCTATGGAATAAGGAGCAGATCTA 122

Qy 509 SerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeu 528
 Db 123 TCTGGAATGAGCCCTGGACACADACTAGACATACTTACAGATAACAGATTA 182

Qy 529 LysSerIleValLeuAsnSerAlaSerLysSerIleValLeuAsnSerAsn 548
 Db 183 AAATCTATGTGAAAATCTGCCAGTAATCTCATGTCAGAAAAGCTAAAAA 242

Qy 549 Lys 549
 Db 243 AAA 245

RESULT 4
 US-09-960-352-8727
 Sequence 8727, Application US/09960352
 Patent No. US20020137139A1
 GENERAL INFORMATION:
 FILE REFERENCE: 16511-006/37-21 (10298) C
 CURRENT APPLICATION NUMBER: US/09/960, 352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO: 8727
 LENGTH: 315
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 37-LIB34-077-Q1-B1-B10
 US-09-960-352-8727

Alignment Scores:
 Pred. No.: 2.32e-22 Length: 315
 Score: 312.50 Matches: 66
 Percent Similarity: 76.24% Conservative: 11
 Best Local Similarity: 65.35% Mismatches: 22
 Query Match: 8.01% Indels: 2
 DB: 10 Gaps: 1

US-09-837-602-2 (1-754) x US-09-960-352-8727 (1-315)

Qy 282 IleProAspCysGlnIleIleSerIleMetAspMetLeuGlnArgGlnGly 301
 Db 14 GTTAAGCACTACAGATGGCTCATTCAGAATGGCTTAACGTTACTCGAGGGGGT 73

Qy 302 LeuArgProIleProGluAlaGluIleGlyLeuAlaVal11LeuMetThrIleSerAsn 321
 Db 74 CATAAGCTTATCCGAAAGGAAATTGGCTTAACGTTACTCGAGGGGGT 133

Qy 322 TyrCysAspProGlnGlyIleProSerThrIleLeuLysThrThrProGlyProSer 341
 Db 134 TACTGTGATACATACGGCCAGTCAAGGAAACACTGGTCAAAC 193

Qy 380 9 380
 Db 314 A 314

RESULT 5
 US-10-269-909-35
 Sequence 35, Application US/10269909
 Publication No. US2003018047A1
 GENERAL INFORMATION:
 APPLICANT: HRUBAN, RALPH H.
 APPLICANT: ARGANI, PEDRAM
 APPLICANT: IACOBUZO-DONAHUE, CHRISTINE
 APPLICANT: MAITRA, ANIRBAN
 TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
 CURRENT APPLICATION NUMBER: US/10/269, 909
 CURRENT FILING DATE: 2003-10-11
 PRIORITY NUMBER: 60/338, 609
 PRIORITY FILING DATE: 2001-10-11
 PRIORITY NUMBER: 60/332, 754
 PRIORITY FILING DATE: 2001-11-19
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 35
 LENGTH: 6456
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-269-909-35

Alignment Scores:
 Pred. No.: 7.74e-12
 Score: 227.50
 Percent Similarity: 36.95%
 Best Local Similarity: 18.78%
 Query Match: 5.83%
 DB: 13
 Gaps: 29

US-09-837-602-2 (1-754) x US-10-269-909-35 (1-6456)

Qy 2 TriPheLeuProAlaAlaGlyProAlaGlyGluProTyArgLeuLeuThrGly 21
 Db 69 TGGTTTTGGAGGTGGAGGCTGGAGGACTGGCCACAGGCTGCCAGGAAATGATT----- 122

Qy 22 ValGluItyrValValIgLyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSerIle 41
 Db 123 -----TTTGTGAAAGATGACTGTGAGCTCATGTCAGCT-----CGTACTGIG 170

Qy 42 SerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsnLeuSerGlnThrAsp 61
 Db 171 GATAACCAACAGCTGTCATAACTATGATCGCT-----ACGGAT 212

Qy 62 GluIleProValLeuThrLeuLysAspAsnSerIlysrGlyThrPheValAsnGluGlu 81
 Db 213 GAGCATTAGTGAAGGATTG-----GGCAGCCATGGAATGGACTTTGTAATGATGTA 266

Qy 82 LysMetGlnAsnGlyPheSerArgThrLeuIysSerGlyArgGlyIleThrPheGlyVal 101
 Db 267 AGGATTCGGAAACAGACTTATCACTTGAAGAACTTGAAACTTGATGAGATTGGATAT 326

Qy 102 PheGlySerIlysrGlyThrArgIleGluIleGluProLeuValAlaCysSerSerCysLeuAsp 121
 Db 327 GATACAAATCTTCTACTGTA-----

Qy 122 ValSerGlySerIlysrGlyThrAlaLeuAsnGlnAlaLeuGlnLeuGlyPheThrValAsn 141

Db 348 GTACAAAGGAAATGAGGTCCTGAGAAGCTCAAGGTTACCATTCAG 407

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/666,6

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Armonia Sequence Listing Engine vers. 1.1

SEQ ID NO: 11287

LENGTH: 442

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: MAP TO ABO13139.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

US-09-864-761-11287

Alignment Scores:

Prev. No.:

Score: 1.99e-12

Length: 442

Matches: 43

Percent Similarity: 78.57%

Conservative: 1

Best Local Similarity: 76.79%

Mismatches: 12

Indels: 0

Gaps: 0

US-09-837-602-2 (1-754) x US-09-864-761-11287 (1-442)

Qy 691 valthryProglalaglyLysbleuprothiilegIlySerIspLeutLeAla 710

Db 269 GTCACATATCTGGAGCAAACTTCACACATCATGGAGTCAATAGCT 328

Qy 711 HISHSAlaarglyAsnThrGluIeuGluIgluIleArgGlnGluValGln 730

Db 329 CATCATGCTCGAAAGATACTAGAACTAGAGTGGCTAAGCAGGAAATGGAGTTAGT 388

Qy 731 AsnGlnHisAlaIalysGluGluSerIeuLeAlaAspAspIeuPheArgTyR 746

Db 389 AGGAGTGGGCCAGAAACTGTTAAATTGCACTTGGCCATT 436

RESULT 7

US-09-864-761-27987

Sequence 27987, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Armonia Sequence Listing Engine vers. 1.1

SEQ ID NO: 27987

Alignment Scores:

Qy 731 AsnGlnHisAlaIalysGluGluSerIeuLeAlaAspAspIeuPheArgTyR 746

Db 389 AGGAGTGGGCCAGAAACTGTTAAATTGCACTTGGCCATT 436

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: SWISSPROT HIT: A147521-1, EVALUUS 3.20e+00

OTHER INFORMATION: EST HUMAN HIT: AF051334-1, EVALUUS 5.00e-58

OTHER INFORMATION: NT HIT: AF051334-1, EVALUUS 5.00e-58

OTHER INFORMATION: US-09-864-761-27987

Alignment Scores:

Pred. No. :	3.35e-12	Length:	114
Score:	205.00	Matches:	38
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.26%	Indels:	0
DB:	9	Gaps:	0
US-09-837-602-2 (1-754) x US-09-864-761-27987 (1-114)			
Qy	691 ValThrTrpGlyAlaGlyLysLeuProHisIleIleGlySerAspLeuIleAla 710	Qy	505 GluGlnHisLeuSer-----GluAsnGluProValAspThrAnsSer 518
Db	1 GTCACATATCTGAGCAGGAAACTCCACATCATTGAGATCATATAGCT 60	Db	505 GluGlnHisLeuSer-----GluAsnGluProValAspThrAnsSer 518
Qy	711 HisIleAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGlnGluMetGlu 728	Qy	519 AspAsnAsnLeuPheThrAspThrAspLeuIleValLeuValLeu 3414
Db	61 CATCATGCTGAAAGAACTACAGAACTAGAGAGAGTGGCTTAAGCAGGAATGGAG 114	Db	3355 GAGGAGCTTTAAAGAGAGAAATTCAACTGAGAGGCCACTGAAACAAACAG 3414
RESULT 8	US-10-369-493-25273	Qy	519 AspAsnAsnLeuPheThrAspThrAspLeuIleValLeuValLeuValLeu 3414
	Sequence 25273, Application US/10369493	Qy	519 AspAsnAsnLeuPheThrAspThrAspLeuIleValLeuValLeuValLeu 3414
	Publication No. US20030233675A1	Db	3415 CAACTCACAGCCTACGTT---GCCAATTAGATACTTAAAGAGCATGAAATTAA 3471
	GENERAL INFORMATION:	Qy	536 AspSerLysSerHisAlaAlaGluValLeuArgSerAsnLysAspGluMetAspAsp 555
	APPLICANT: Cao, Yongwei	Db	3472 GCAGCTCGAGTTGAGAGACTACGAGGAAATTCAGCAAGGAAAGCCATAACCGAG 3531
	APPLICANT: Hinkle, Gregory J.	Qy	556 -----ValAlaIleGluAspGluValLeu-----GluGlnLeuPhePhe 568
	APPLICANT: Slater, Steven C.	Db	3532 GAATATCTCAATTAAATGATGAGATTAATGTAATGAACTCAACAGAAATTAAG 3591
	APPLICANT: Chen, Xianfeng	Qy	569 AspThrLysProGluLeuGluGluLeuAspValGlnLys-----GlnGluGluAsp 586
	APPLICANT: Goldman, Barry S.	Db	3592 AAAAAAATGACGAACTGGAGCGAACTGGAGACTTCAGGGAAACAA 3651
	APPLICANT: Hinkle, Gregory J.	Qy	587 ValAsnValArgLysArgPro-----ArgMet 595
	APPLICANT: Chen, Xianfeng	Db	3652 TCAATTGAAAGTCAGAGATTGATCAGAGATTGCAATTAAAGCTGAAATTAAAGCTGAAAG 3711
	TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES	Qy	596 AspIleGluIleThrAsnAspThrPheSerAspGluAlaValProGluSerSerLysIleSer 615
	FILE REFERENCE: 38-10 (52052)B	Db	3712 AAGAACGAAACGAGAACGCC-----AGTTTATTGGAGTCATCAA-----AGT 3756
	CURRENT APPLICATION NUMBER: US/10/369,493	Qy	616 GluGluAsnGluIleGlyLysIleGluSerAspGluLeuLeu----- 635
	CURRENT FILING DATE: 2003-02-28	Db	3757 GTAGAATAGAAACGGTAAAAAATTAAAGAAATACAAAGCAGTGTAACTTTAAAGAAAG 3816
	PRIOR APPLICATION NUMBER: US 60/3360,039	Qy	636 GluIleSerAsn---AsnAspLysIleGluLeuAspSerGluMetLeuProIleSleu 654
	PRIOR FILING DATE: 2002-02-21	Db	3817 GAATGTAGTGAATTGGAGACAACTCAG-----GCCTAGAGATAAACTGAAAG 3873
	NUMBER OF SEQ ID NOS: 47374	Qy	655 IleLeuIleGluPheArgSerLeuValLeuIleAsnSerThrSerGlnProSerGly 674
	SEQ ID NO 25273	Db	3874 TCGGAGCTACAGAGGATTCGGAGAAAGTAATGCTAAAGACGCTGAA 3933
	LENGTH: 5373	Qy	675 IleAsnAspAspIleGlyGlnLeuIleAsnPhiLysIlePhiLysIlePhiLys 694
	TYPE: DNA	Db	3914 CTAAAATTCAATTGAAAGATCAATTATTCAGGCCAAAGGAAATCAGATCT 3993
	ORGANISM: Saccharomyces cerevisiae	Qy	695 GlyAlaGlyLysIleuProHisIleIleGlySerAspLeuIleAlaHisIleAlaArg 714
	US-10-369-493-25273	Db	3994 GAGTTGCTGATGTTGAAAG-----ACATCTTCGAGGAAGAA 4032
	Alignment Scores:	Qy	715 LysAsnThrGluLeuGlu-----GluTrpLeuIleGluGlnMetGluValGlnAsnGlnHis 733
Pred. No. :	3.99e-07	Db	4033 AAAATTGCGAGGAGCAATTGGAAAAATTGAAATAATCAAAATCAGGCC 4092
Score:	179.50	Qy	734 AlaLysGluGlu----- 737
Percent Similarity:	40.91%	Db	4093 TTGAAAGGAGAAAGCTACTTAAGGAACTCTCAACAAAGATATTCT 4152
Best Local Similarity:	23.15%	Qy	738 -----SerLeuAlaAspAspLeuPheArg 745
Query Match:	4.60%	Db	4153 GAAAAGATCAAATCTGAACTTGGAAAGATGAAATTAAATTGG 4188
DB:	12	Qy	RESULT 9
	Gaps: 19	Db	US-09-801-368-51
		Qy	Sequence 51, Application US/09801368
		Db	Patent No. US2002028250A1
			GENERAL INFORMATION:
			APPLICANT: Busby, Robert
			APPLICANT: Busby, Robert

APPLICANT: Hecht, Peter	Qy	502 LysAsnLysGlnGlnHisLeu-----
APPLICANT: Holtzman, Doug	Db	1594 ArgTATAGTGTAAAGACTTTTACTGGACAAAATTTATCCTCTGAAGAAAACAGGG 1653
APPLICANT: Madden, Kevin		
APPLICANT: Maxon, Mary		
APPLICANT: Milne, Todd		
APPLICANT: No. US202128250A1man, Thea		
APPLICANT: Royer, John		
APPLICANT: Salama, Sofie		
APPLICANT: Sherman, Amir		
APPLICANT: Silva, Jeff		
APPLICANT: Summers, Eric		
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi		
FILE REFERENCE: 10972-147		
CURRENT APPLICATION NUMBER: US/09/801.368		
CURRENT FILING DATE: 2001-03-07		
PRIOR APPLICATION NUMBER: US 09/487,558		
PRIOR FILING DATE: 2000-01-19		
PRIOR APPLICATION NUMBER: US 60/160,587		
PRIOR FILING DATE: 1999-10-20		
NUMBER OF SEQ ID NOS: 440		
SOFTWARE: Patentin version 3.0		
SQO ID NO 51		
LENGTH: 4437		
TYPE: DNA		
ORGANISM: <i>Saccharomyces cerevisiae</i>		
US-09-801-368-51		
Alignment Scores:		
Scored. No.:	3.36e-07	Length: 4437
Core:	179.00	Matches: 108
Conservative:	38.92%	Conservative: 87
Best Local Similarity:	21.56%	Nimatches: 167
Query Match:	4.59%	Indels: 139
BB:	10	Gaps: 21
US-09-837-602-2 (1-754) x US-09-801-368-51 (1-4437)		
Y	324 AspProGlnGlyHisProSerThrGlyLeuLysThrThrProGlyProSerLeuSer 343	Qy 620 -----IleGlyLysBrgGluLeuLysGluAspSerLeuTrpSerAlaLysGlu 636
Db	1156 AATCCACAGGTCA-----AGTCTCTACTGAAATAATTAGCT 1194	Db 2134 TATGACAGAGTTCCATACTAACTCAACTGAGATTATGAAATTATTAAGAA 2193
Y	344 GluGlyValSerValAppGlyLeuMetProSerAlaProValAsnThrThrThr 363	Qy 637 IleSerAsnAsnAspLysLeuGlnAppAspSerGluMetLeuProGlyLysLeuLeu 656
Db	1195 AAAGGAAATCTAAACACTGAAACTGTTAACAACTCTCA----- 1251	Db 2194 GTTCTCTCTCATGAG-----GAAATGCAACAAATGCTTTTAA 2235
Y	364 ValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGlu 383	Qy 657 ThrGluPheArg-----serLeuValleLysAsnSerThrArgAsnProSer 673
Db	1252 ---CTACCCACTTCGGATGATAAAGGTAAATTATGGATAAATTCAAGAAAGGCCAA 1308	Db 2236 ACAAGTCCAATAATTAGAACTAACCTTACAGATAAAGGAAGTAATAATTAAATTATTCTCTAAC 2295
Y	384 IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThrVal 403	Qy 674 GlyIleAsnAspAspSerThrGlyGlnLeuLysAsnPhenylsLysSerValThrTyr 693
Db	1309 ATAGGGCTCTAGGCCAATAACGGTAGCTTATGTAACGTCTCAAGAAACCTCATCTTA 1368	Db 2296 CCCATACAGAAAATGAAAGCAAG-----AGTATGTTTCAAGTGTAGAA 2343
Y	404 LysGluSerCysLysThrSerSerAsnSerAsnSerMetAlaProValLeuAlaLys 423	Qy 694 ProGlyAlaGlyLysLeuProHisIleIleGlyGlySerAspLeuLeAlaHisHeAla 713
Db	1369 AAA-----TCGAAATTGAGGACTGCTACCTTAACCGTACAAAACGGCAGAT 1413	Db 2343 ----- 2343
Y	424 MetArgPheProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsnLysSerLys 443	Qy 714 ArgLysAsnThrGluLeuGluGluLysLeuGlnLysGlu----- 732
Db	1414 GTAAATTAACCTCTCCATCTCTCATCA-----CCCGCAATAACCAAACGCA 1464	Db 2344 GATGAGGGACTGAAATTGATTCATACTCATGCTAGGAAATGCCCTATAACAAACCGAA 2403
Y	444 AspArgAlaSerGlnGlnGlnThrAsnSerIleArgAsnTyrPheGlnProSerThr 463	Qy 733 ---HisAlaLysGluGlu-----SerLeuAlaAspAspIlePheArgTyrAsnProTyr 749
Db	1465 AACAGAACTTGGAGGTCTACACCA----- 1491	Db 2404 CTGGCACCAAAAGAGCACGCTCCGAAATAACTCTCAGGAGCCCTTA 2463
Y	464 LysBrgGluLysGluArgAspGluGluLysBrgGluMetSerCysLysSerAlaArgLys 483	Qy 749 F 749
Db	1492 -----GAAGATAACCTAAATACTTCACCCGGCTCTTTAAA 1533	Db 2464 T 2464
Y	484 GluThr-----SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrp 501	RESULT 10
Y	1534 GAAAGCTATCCGATGATGTTATATCCAGAACAGACTCCGTTGCGGTAAATAATCAA 1593	US-10-369-493-45841 ; Sequence 45841, Application US/10369493 ; Publication No. US20030233675A1 ; GENERAL INFORMATION

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Qy	216	GlnGluArgLysClnIlePhePhePhePheLysThrPheIlePheLeuasnAlaLysGlnHis	235
Db	1944	GGGGCAGAAAG-----AAAGGTCACTCTTCCAGACAGTGTCTCCACCGG	1994
Qy	236	LysLysLeuSerAlaValValPheGlyGlyGluLalaArgIleThrGluGlu	255
Db	1995	GAAATCTGAA-----AAGCTGATGAAACACCTG	2024
Qy	256	AspGluGluGluHisAsnPhePhe-----LeuAlaProGly	267
Db	2025	AGGACACCCCATCCTCACTTGTGGCTGCACTATCCCCTGAGGGAAAGGCTCCAGGG	2084
Qy	268	ThrCysValValAspThrGlyIleThrAsnSerGlnThrLeu-----	281
Db	2085	-GTTATGGAACACCCCTGGATGCAACCAAGTGCGATGCAACGGAGTGCTGGAG	2138
Qy	282	-IleProAspCysGlnLysLysIlePheIleGlnSerIleMet-----AspMetLeuGln	298
Db	2139	GGPATTCGCACTCGTGAAGGGCTTCCCCAACCGATTCTTATGGGACTTCCGGCAG	2198
Qy	299	Arg---GlnGlyLeuWargPro-----IleProGlu-----	307
Db	2199	AGGTATCGAAATCTGAACCCGAGGCTTCCCTGAGGGCATTATGATAGCAGAAA	2258
Qy	308	--AlaGluIleGlyLeuAlaValIle-PheMetThrThrThrLysAsn-----	321
Db	2259	GCGCTGAAAGTCGCTGGCTGGCTTGACATTGACCAACACCAGTACAAGTTGGCAC	2318
Qy	322	-----	327
Db	2319	ACCAAGGTGTTCTCAAGGGGGCTCTGGGGCTCTGGGGAGATGCGAGATGAGG	2378
Qy	327	Y-----HisProSerThrGlyLeuIle-----	334
Db	2379	CTGAGCCGCATCATCACCGAATCAGCTAAGCCGAGGCCAGGTCATGGCATGTGAG	2438
Qy	335	-----ThrThrThrProGlyPr	340
Db	2439	TTCAGAGAGATGTTGACGCCCTGCTGTTATCAGCTGAAACATCCGGCC	2498
Qy	340	0SerLeu-SerGlnGlyValSerValAspGluIleMetProSer-AlaProValAsn	359
Db	2499	TTCATGGGGTCGAAATTGGCGTGTATGAGGCTACTTCAAGGTCAGGCCGCTG	2558
Qy	360	ThrThrThrValAlaAspThrGluGlnIalaAspThrItpAspLeuSerGlu	379
Db	2559	AAGGC-----GCGAGAGAGAGGGATGCCAAATGAAAGAGGAGTGTGGG	2609
Qy	380	ArgProLys-----GluIleLysValSerLysAspArgAlaSerGlnGlnThrAsn	393
Db	2610	CGACTCAAAGATGCACTAGAGAAAGTCAGGCTCGCCGCAAGGCCAGAAGATG	2669
Qy	394	ArgMetLeuSerGlnAspAlaProThrValIleValysGluSerCysLysThrSerSerAsnAsn	413
Db	2670	GTTGTCCTGTCGAGAGAGATGACTGAGCTCAAGTCAGGCCAGGGAAACAGAAC	2729
Qy	414	AsnSerMetValSerAsnThrLeuAlaLysMetArgIleProAsnItyrGlnLeuSerPro	433
Db	2729	-----	2729
Qy	434	ThrLysLeuProSerIleAsnLysSerLysAspArgAlaSerGlnGlnThrAsn	453
Db	2730	-CTGGCAAGATGGCGAGGAGCTGGCTGCGAGGCCAGGCGCCAGCAG	2759
Qy	454	SerIleArgAsnItyrPheGlnProSerThrLysLysArg-----GluArgAspGlu	470
Db	2760	CTGATCAGAACAGATCAGTGGAGCCANGTGAAGGAGATGACCGAGGCTGGAG	2819
Qy	471	GluAspGlnGluMetSer-----SerCysLysSerAlaArgIleGluThrSerCys	487
Db	2820	GAAGCCAGGAGCTGAGTCGCCGAGCTGAGGCCAAAGAGGCCAAAGCTGGCTGAGGCTGGAG	2879

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488	Ser--LeuLeuGluGlnGlnThrGlnProAlaThrProSerLeuTrpLys--AsnLygGlu	505	TYPE: DNA
2880	TCAGAGCTCAAGAAGATATCGATGACCTGGCTGACCTGGCCAGGTGGAGAGGA	2939	ORGANISM: <i>Candida albicans</i>
US-10-032-585-6646			
506	GlnHisLeuSerGluAspGluProValAspThrAsnSerAspAsnAsnLeuPheThrAsp	525	Alignment Scores:
2840	AAGCACGAACAGAAACAG--	2960	P-req. No.: 9
Db			Length: 9.65e-07
DY			Matches: 96
Db			Percent Similarity: 41.50%
526	ThrAspLeuLysSerIleValLeuAsnSerAlaSerLysSerHisAlaAlaGluLysLeu	545	Best Local Similarity: 21.77%
2961			Query Match: 4.51%
Db			DB: 13
546	ArgSerAsnLysLys--ArgGluMetAspAspValAlaIle	558	US-09-837-602-2 (1-754) × US-10-032-585-6646 (1-5641)
Db			
Db			
3015	ACCAAGGGAGGAGGAGGCTTCAGAGGCCACCAGG2AGGCCCTAGATGACCTTCAGGT	3074	Qy 367 ThrGluSerGluGlnAlaAspThrTrpAsp--LeuSerGluArgProLygGluLle
DY			Db 22236 ACCAAAAACGAAATGCCGAAAGGAAATGATAAAGAATTGAGAAAGATTGAGAACTA
Db			22959
559	GluAspGluValLeuGluGlnLeuPheLysAspThrLysProGluLeuGluLeAspAla	578	Qy 385 Lys--ValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThr
3075			Db 2296 ACTTAATCTTCCACCAAACTCGAAAAGCTGAAAGACAAGGAAAGAAATTGCCCAA
Db			23559
579	LysValGlnLysGlnGluGluAspValAsnValArgLysArgProArgMetAspIleGlu	598	Qy 403 VallySglySerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAla
3126			Db 2356 ATCCAAGGAGATCACAACTGCTTAATGAAAGTTCTGGTCAGGCCAACAGTTATGC
Db			2415
599	ThrAsnAspThrPheSerAspGluAlaValProGluSerSerLysSerGlnGluAsn	618	Qy 423 LysMetArgIle-----
3186	CGA-----	3188	Db 2416 GGCATAAAGGCTCGGACGAAAGAGCAGCAGAACTATTCAGGCCGGATCAGACAGAACTA
DY			24747
619	GluLleGlyLysLysAspGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSer	638	Qy 431 -----LeuSerProThrLysLeuProSerIleAsnLygSer
Db			Db 24746 CAAGGGCTTTGAAAAAGGGTAACACTCTGAAAGCACATTGAGCAATGAAAGAAAA
3189			Qy 443 LysAspArgAlaSerGlnGlnGlnGln-----ThrAsnSerIleArg
Db			Db 2536 CTTGATTCCAGAACAGAACAGGCCAAAGAACAAAGAACATGAGCTAGA
DY			2599
639	Asn--AsnAspLysLeuGlnAspAspSerGluMetLeuProLysLeuLeuLeu	656	Qy 457 AsnTyPhe-----
3240			Db 2596 GACATATCCATCTAAAAAACGCTGAAAGCTGAAACTCAAACAACTGAA
Db			26547
657	ThrGluPheArgSerLeuValLeuLysAsnSerThrSerArgAsnProSerGlyIleAsn	676	Qy 468 ArgAspGluGluAsn-----GlnGluWetSerSerCysLysSerGlnGlu
3295			Db 2655 AGAGAGTTAAATTTGACTTATGAAATTGAAACACTAAAG--GATTGAACTTA
DY			2712
677	AspAspTygGly--GlnIleuLysAsnPhiLysPhiLysLysValThrTyrProGly	695	Qy 486 SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpAsnLysGlu
Db			Db 2713 CAAATTAATTTGAAATCAATCAAAT
3324			Qy 487 :-----AATGAAATCTGAAACGAAACTGAAAG--AATGAACTCAACAGAAATA
DY			2766
696	AlaGlyLysLeuProHisIleLeuGlyLysSerAspLeuIleAlaHisIleAlaArgLys	715	Qy 506 GlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPheThrAsp
Db			Db 2761 AATGAAATTGAGTAAGAAA-----ATCGAACTCTGACTCAAGATAATAATTATGCC
3369			2811
DY			Qy 526 ThraspLeuLysSerIleValLeuLysAsnSerIleValLeuGluAspValAlaLysGlu
716	AsnThrGluLeuGluGluIleValLeuGluMetGluValGlnAsnGlnHisIleAlaLys	735	Qy 545 LeuArgSerAsnLysLysArgGluMetAspAspValAlaLysGluValLeuGlu
Db			Db 2875 TTGACATCTGATCATGTTGCTGATCATGTTGAAAGAACTGAAATCTGAA
3381			293
DY			Qy 565 GlnLeuPheLysAspThrLysProGluLeuGlu--IleAspValLysValGlnGlyGln
736	GluGluSerLeuAlaAspAspLeuPheAsp	745	Db 2935 GAAACAGTAAAG--GCCAAAGAAGAGTGGAAACACTTACCACTGAAAGATTGATAATCT
Db			299
3432	GTGGAGAACACTGCTCACACCTGACCCGG	3461	Qy 584 GluGluAspValAsnValArgLysArgProArgMetAspIleGlu-----
DY			Db 2992 GAAAGGAATGAAAGAACACAACTAAATAAAATGAAATTGAAATCTAAAT
3502	ATTACTGATTCTACCAATGAAAGGATGAACTTAAAGGAAATTAGAGGATGAACTTAA	3505	305
SEQ ID NO: 8000			599
SOFTWARE: PatentIn version 3.1			5641
SEQ ID NO: 6646			5646
GENERAL INFORMATION:			5646
APPLICANT: Terry, Roemer D.			5646
APPLICANT: Charles, Boone			5646
APPLICANT: Howard, Bussey			5646
APPLICANT: Gene Disruption Methodologies for Drug Target Discovery			5646
FILE REFERENCE: 10182-005-999			5646
CURRENT APPLICATION NUMBER: US/10/032,585			5646
CURRENT FILING DATE: 2001-12-20			5646
NUMBER OF SEQ ID NOs: 8000			5646
SEQUENCE: Sequence 6646, Application US/10032585			5646
PUBLICATION NO. US20030180953A1			5646
APPLICANT: Bo, Jiang			5646
APPLICANT: Charles, Boone			5646
APPLICANT: Howard, Bussey			5646
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NUMBER OF SEQ ID NOs: 8000			5646
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APPLICANT: Bo, Jiang			5646
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APPLICANT: Bo, Jiang			5646
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APPLICANT: Charles, Boone			5646
AP			

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Qy 610 GluSerSerlys----IleSerGlnGluAsnGluIleGlyLysArgGluLeuIys 627
 ::|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 db 3112 AAATCCAAATAAAGAAATCTCCATAAAATTCAAGATTAACTGAGAAACT 3171
 Qy 628 GluAspSerLeuThrSer----AlaArgGluIleSer 638
 db 31172 GAAAAGATCTCCAAAGCAAAAGATGATAAAATTGAAAGCTGAGACCAAAATCA 3231
 Qy 639 AsnAsnAspIysLendIaaDAspSerGluMetLeuLeuLeuLeuLeuLeuIys 658
 db 3232 ATATTGATAATCTAAATTAGAAATTCTCTAGTTTACATCGAAGTTG 3279
 Qy 659 PheArgSerLeuvalIleSerAsnSerThrSerArgAsnProSerGlyLeAsnAsp 678
 db 3280 ----AAAGAACCGCAAGAAATCTCAACTTCTGAAATCTCAAATGAA 3318
 Qy 679 TyrGlyGlyIleu----LysAsnPheIleuLysValThrTyrProGlyAlaGly 697
 db 33119 CACTCTTCACCTTCTGAAATCTCAAATGAA 3372
 Qy 698 LysLeuProIleIleGlyGlyIleuSerAspIleuIleAlaIleGlyAsnThr 717
 db 3373 AAAACTCTCAATGATGCCAACCTTCAGCAAGATTGAGGCAAAAGGCCACTGT 3432
 Qy 718 GluLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGlu 737
 db 3433 GAAATTGAACAACTAACATCACCGACTAACACATCACCGACTAACAGCAAAG 3492
 Qy 738 Ser 738
 db 3493 TCA 3495

RESULT 13
 US-10-369-493-45712
 ; Sequence 45712, Application US/10369493
 ; PUBLICATION NO. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (5202) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 45712
 ; LENGTH: 5787
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-45712

Alignment Scores:
 Pred. No.: 1.59e-06 Length: 5787
 Score: 174.00 Matches: 153
 Percent Similarity: 37.31% Conservative: 116
 Best Local Similarity: 21.22% Mismatches: 258
 Query Match: 4.46% Indels: 195
 DB: 12 Gaps: 37

US-09-837-602-2 (1-754) x US-10-369-493-45712 (1-5787)
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 db 1713 TTCAAGATTTAAATAATGG 1733
 Qy 158 ThrIleThrIle----CysAlaLeuIleCysGlyArgProIleVal---Lys 173
 db 2700 TACGCAAGGACTTGTAAATCAGGGAAA-----GAGAAATTAGAAAAT--GA 2747

Db 1734 CATTGAAACACTATGCTGGGATGTGGAAGCTGGTTATACACTGTGGAAGCTGGTTATCCAAAAAA 1793
 Qy 174 ProGluIysPhe-ThrGluIleLeuLysAlaValAlaGlnSerLysLysGlnProGlnIly 193
 db 1794 CAAGATCCTTTAAAGCTATAATCTCTGCTCTTGTCTTCACAAACGATATCAT 1853
 Qy 193 eGluSerPheTyProProLeuAspGluProSerIleGlySerLysSerValAlaAspLeu 213
 db 1854 TTCAAACGTGTCAGCCAGGGGAAATACT---TCTAGTGCTGGTGTGGAGGCCAA 1910.
 Qy 213 r---GlyArgGlnGluArgLysGlnIlePheIysGlyLysThrPheIlePheLeuAsnAl 232
 db 1911 CATCCCAACCAAGCTAAAGTAAGAAATCACTGACAAACTACCTTC---AAGACTACATC 1967
 Qy 232 aLyGlnIlyLysIleAsnSerLeuSerSerAlaValAlaValPheGlyLysIleGluAlaArgLeu 1 252
 db 1968 ATCACGCCATAGAGAA----CAGCAGAT 1991
 Qy 252 ethrGluGluAsnIysLys----GluGluHisAsnNpheIleuAlaProGlyThrCysBya 270
 db 1992 AACATTAACAAATCAACTAGCTCTAACCAACATTTGTT----CTGTGAT 2042
 db 270 IvalAspThrGlyIleIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpI 290
 db 2043 AATTCACAAACCTGAAAAAGTCGAAACATTAAACAGA----- 2082
 db 290 eGlnSerIleMetAspMetLeuGln-----ArgGlnIlyLeuIleArgProIlePr 306
 db 2083 -AGGTAAATCTTAGTCATTACCTGTAATGGTTGTAATGGGTATAGACTGCCAG 2141
 Qy 306 oGluAla-----GluIleGlyLeuAlaValIlePheMetThrThrAsnTyrcy 323
 db 2142 AGAGTTACCCAAATAGGATAGGATTCAGGGTATAGGATCTGGT--- 2199
 Qy 323 sAspProGlnGlyHisProSerThrGlyIleIlySerThrThrProGlyProSerLeuSe 343
 db 2200 -----TATCCCTGAAATTCACCAACCAAGCTACGACTTCTAGTTCTAAATTAAGGC 2246
 Qy 343 rGlnIlyValSerValAspGluIyLeuMetProSerAlaProValAsnThrThrThr 363
 db 2247 CAGTACCCAAACAAACATGTAATGGTTCTAACTGCAACTGGTACATAAGATTTA 2306
 Qy 363 r---ValAlaAspThrIrglu-----SerGluGlnAlaAspThrTrpAspIle 377
 db 2307 TAAATGTTGAAATCTAAAGCTGAGPATGCGAGATGTTG--- 2358
 Qy 377 uSerGluIyArgProIysGluIleIysValSerLysMetGluGlnIlySpheArgMetLeuSe 397
 db 2359 -----GAAAAACAAAAAGATGTTAACATGATAATAATTGATTAACATGAACTAACTAACAGCAACTAT 2414
 Qy 397 rGlnAspAlaProThrValIlyGluUserCys----- 410
 db 2415 ACGGAGTTACACAGTAAGAAATAACGTCACATCTAACCTGCAACTGGTACATAAGATGAA 2474
 Qy 410 rSerAsnAsnAsnSerMet--"ValSerAsnThrLeuAlaLysMetArgIleProAsnTy 429
 db 2475 GGTGATTTGTTGAAATCTCAGATGATACATAGCTGAACTGGTGAAGG---GAGATCCTGGTT 2531
 Qy 429 rGlnIleSerProThrIlyLeuProSerIleAlnIlySerLysBspArgAlaSerGlnG 449
 db 2532 TAATTATTATTCAGGATCAAGCCACCTTTAACATCATCAATGACATGACCAAGACCAA 2591
 Qy 449 n-----GlnGlnThrAsnSerIleArgAsnTyrPheGlnPro---SerThrIlyB 465
 db 2592 AAAATTCACGAGAAATAATAATGAGAAATGAAATGAAATGAAATGAA 2651
 Qy 465 sArgGluArgAspGluGluAsnGlnGluMetSerSerCysLysSerAlaArgIleGluTh 485
 db 2652 GAAGTTGGAAAGAAAGACCAAAACTGAAATCTCAAGAAATGAAATGAA 2699
 Qy 485 rSerCysSerLeuLeuGluGluIlyLeuProSerIleTrpLysAsnLysGlnProAlaThr 505
 db 2700 TACGCAAGGACTTGTAAATCAGGGAAA-----GAGAAATTAGAAAAT--GA 2747

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223 LysGlyLysThrPheLeuIleAlaLysGlnHisLysLysLeuSerSerAlaVal 242
 Qy 2742 AATACAAAGATT-----GACTCTCTGAGATGAGAACACGCCAAAGGA 2792
 Db 2443 ValPheGlyGlyGluIleArgLeuIleThr----- 253
 Db 2793 ATGGATATCAAGGGCACAAAATTGAGACCTCAAGAGGATCATCTGATGCT 2852
 Qy 254 GluGluAsnGluGlugluHiAsnPheLeuAlaProLysValValAspThr 273
 Db 2853 GAAAGAAACAGAGAGAGACTCTCTAGCGAGACGAGCTGTGATAAAGACAC 2912
 Qy 274 GlyIleIleAsnSerGlnThrLeuIleProAspGlyGlnLysLysLeuPro 293
 Db 2913 ACCATCATGGATTAAAGATGCACTCT-----LeuArg 303
 Qy 294 MetAspMetLeuGlnIargGlnGly----- 3044
 Db 2967 ACTGATGGTGTGATAAGCTCTCTGGAAAGAGAGAGGTTTACTCTTGGAAAGTTAGA 3026
 Qy 3004 ProIleProGluAlaGluIleGlyLeuAlaVallePheMetThrThrAsnTyrCys 323
 Db 3027 AAAGTGTGAACTAA----- 3044
 Qy 324 AspProGlyLysProSerThrGlyLeuLysThrThrProGlyProSerIleSer 343
 Db 3045 -----GAAAGAGCAAGGATCTCAAAACAAACA---TGTAAAAGTAGCTC 3089
 Qy 344 GlnGlyValSer---ValAspGluLysLeuMetProSerAlaProValAsnThrThrThr 362
 Db 3090 GATGGCTTATCTGATATTGAGAATTCCTAAGAAAGCAGCAGCTGAACACTCT 3149
 Qy 363 TyrValAlaAspThrClusUserGluGlnAlaAspThrTriAspLeuSerGluAspProlys 382
 Db 3150 -----GAAGATGATDAAAAGCAGCCAAAGAGAAACTCTAAGAAAGAATCTTAAG 3203
 Qy 383 GluIle-----LysValSerLysMetGluGlnLysPheArgMetLeuSer----- 397
 Db 3204 GACTTAAGAAAAAACTTAATAATGGACAACAGTATAATCTCATGTGGACT 3263
 Qy 398 GlnAspAlaProThrValyGluUserCysLysThrSerSerAsnAsnSerMetVal 417
 Db 3264 GAAAAGTACTGTGGAGAGAAATTGICATTTCTTAAGGCATAAACAAATTAAAG 3323
 Qy 418 SerAsnThrIleAlaLysMetAspSerProAsnIleProSerProThrLysLeuPro 437
 Db 3324 AATGGAAACAACTGATGGAGAAAG----- 3347
 Qy 438 SerIleAsnLysSerLysAspArgAlaSerGlnGlnIleAsnSerIleArgAsn 457
 Db 3348 AAAAGTAAAAATATGAGATAAAACTTCAAAAGAG-----GATAATATCTGT 3401
 Qy 458 TyrPheGlnProSerThrLysLysArgGluLysArgAspGluLysGlnGluMetSerSer 477
 Db 3402 TATGCTGAGAATGCTCAACGCCAAAGGAGAGATGTTGACTCTGAGGATAAAAGCT 3461
 Qy 478 CysIleSerAla-----ArgIleGlnSerCysSerIleLeuGluGlnIleGlnPro 495
 Db 3462 AAGAATGGAGGATATGTTAGAGAGAAAGGTCGAAGTGTGCTGGAAAG----- 3512
 Qy 496 AlaThrProSerLeuIleProSerAsnLeuIlePheThrAspThrAspLeuIleSer 515
 Db 3513 -----AGTTCAAGGAGAGAGAGATGTTGACTCTGAGACTGAGAAATAATTC 3563
 Qy 516 ThrAsnSerAspAsnSerAsnLeuIlePheThrAspThrAspLeuIleSer 531
 Db 3564 ATGAAAAGAATGTTGAACTCTGATAAGAGACTAAAGGAAACTGAGGAA 3623
 Qy 532 -----ValAsnSerAlaSerAsnSerIleSerLysSer 539
 Db 3624 AGAAGAAATTAAAGTCAAAAGAGAAATACTAAGGAAATCAAGTGGCTCATCATCT 3683

540 HisAlaAlaGluLysLeuArgSerAsnLysLysLeuArgGluMetAspAspValAlaIleGlu 559
 Db 3684 GATGCTGAGAAAGTCTCAAGATATAAAAGGAGCAAGACTCATCTAAAGG 3743
 Qy 560 AspGluValLeuGluGlnLeuPheLeuAspAspThrLysProGluLeuGluLeuAspVal 579
 Db 3744 AAGGAGCTATT----- 3785
 Qy 580 ValGlnLysGlnGluGluLysAspValAlaLysGlyAspProArgMetAspIleGluThr 599
 Db 3786 ACAACACTAAAGGAAAGCTGACATTACATCTCATCTCTGATATAAGAGAT 3845
 Qy 600 AsnAspThr----- 600
 Db 3846 GATATTCGAAATCTCTATGGTGAAGGAGCAGCTGAGAGAAATTAAGCCTGACT 3905
 Qy 612 SerLysIleSerGlnGluAsnGluIleGlyLysAspArgGluLeuLysGluAspSerIle 631
 Db 3906 GAAATTAGTGTGCTCTCACATCTGATTTGCAATCTCAGGGATGAGCCITA 3965
 Db 632 TrpSerAlaIleSerGluIleSer-----AsnAsnAspLysLeuGlnAspAspSerGlnMet 649
 Db 3966 TCTAAATCAGTGCCTGACAGTGGATGATGATGATGATGATGATG 650
 Qy 650 LeuProLysIleLeuLeuIleThrGluPheArgSerLeuValIleLysAsnSerThrSer 669
 Db 4026 ATTACCAAGAAGATGCTTTAGAGAA----- 670
 Qy 670 ArgAsnProSerGlyIleAsnAspSer-----TyrGlyIleLeuLysAsnPhenyls 686
 Db 4071 TCGATGAGGATGCTCTCAGATGATGAGCTGAGATGAGCTGAG 685
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 Db 4131 CAAATGAGAA-----AACCAAGGAGATGAGAAAGAAATGAGAA 706
 Qy 706 SerAspLeuIleAlaIleHisIleAlaArgLysAsnThrGluLeuGluIleArgLys 725
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 Qy 726 GluMetGluValGlnAsnLysAsnThrGluLeuGluIleArgLys 737
 Db 4245 AAATTGACTGTGAGTGAAGGAGAAATCTGGAGAATCTGGAGAGAA 4280

Search completed: January 6, 2004, 16:42:12
 Job time : 713 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.		Gencore version 5.1.6		Sequence 5, Appli	
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1 protein - nucleic search, using frame_plus_p2n model					
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Maximum Match 100%		26 155.5 4.0 30549 4 US-09-134-132		Sequence 22, Appli	Sequence 4, Appli
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-OOPTM=0 -PATENTS=NA -QFMT=fastp -SUFFIX=runat -MINMATCH=0.1 -LOCPCL=0		38 150 3.8 1383 2 US-09-005-069-82		Sequence 26, Appli	Sequence 26, Appli
-OOPTM=0 -PATENTS=NA -QFMT=fastp -SUFFIX=runat -MINMATCH=0.1 -LOCPCL=0		39 150 3.8 1383 4 US-09-171-156A-8		Sequence 26, Appli	Sequence 26, Appli
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-OOPTM=0 -PATENTS=NA -QFMT=fastp -SUFFIX=runat -MINMATCH=0.1 -LOCPCL=0		42 149.5 3.8 2617 1 US-08-430-024-1		Sequence 26, Appli	Sequence 26, Appli
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ALIGMENTS					
RESULT 1 US-09-300-008B-1					
; Sequence 1, Application US/093000008B					
; Patent No. 6458534					
; GENERAL INFORMATION:					
; APPLICANT: Concanon et al.					
; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE					
; FILE REFERENCE: 9924-0003-228					
; CURRENT APPLICATION NUMBER: US/09/300, 008B					
; CURRENT FILING DATE: 1999-04-27					
; PRIOR APPLICATION NUMBER: US 60/083, 269					
; PRIOR FILING DATE: 1998-04-27					
; NUMBER OF SEQ ID NOS: 64					
; SOFTWARE: FastSEQ for Windows Version 3.0					
; SEQ ID NO 1					
; LENGTH: 4386					
; TYPE: DNA					
; ORGANISM: Homo sapien					
; FEATURE: CDS					
; LOCATION: (26) . . . (2287)					
; US-09-300-008B-1					
SUMMARIES					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution. and is derived by analysis of the result being printed.					
Issued_Patents_NA.*					
1: /cgn2_6/ptodata/1/ina/5A COMB. seq.*					
2: /cgn2_6/ptodata/1/ina/5B COMB. seq.*					
3: /cgn2_6/ptodata/1/ina/6A COMB. seq.*					
4: /cgn2_6/ptodata/1/ina/6B COMB. seq.*					
5: /cgn2_6/ptodata/1/ina/PCTUS COMB. seq.*					
6: /cgn2_6/ptodata/1/ina/backFiles1.seq.*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution. and is derived by analysis of the result being printed.					
SUMMARIES					
; Query					
; Match					
; Length					
; DB ID					
; Description					
; Sequence 1, Appli					
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; Sequence 79, Appli					
; Sequence 7, Appli					
; Length: 4386					
; Matches: 753					
; Conservative: 1					
; Mismatches: 0					
; Gaps: 0					
; Query Match: 4					
; DB: 4					
; Best Local Similarity: 99.87%					
; Percent Similarity: 100.00%					
; Query Match: 99.92%					
; DB: 4					
; US-09-837-602-2 (1-754) x US-09-300-008B-1 (1-4386)					
; 1 MetryptylsLeuLeuProAlaAlaGlyProAlaAlaGlyroAlaGlyroAlaGlyLeuLeuThr 20					

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Qy 741 AspAspLeuIleArgTyrAsnProTyrLeuIleArgArgArg 754
 Db 2246 GATGATCTTTAGATACATCCATTAAAAGGAGAGA 2287

RESULT 2
 Sequence 2, Application US/08938105-2
 Patent No. 6353151
 GENERAL INFORMATION:
 APPLICANT: Leinwand, Leslie A.
 ADDRESS: 1700 Lincoln St., Suite 3500
 CITY: Denver
 STATE: CO
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,105
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Crook, Wayne L. M.
 REGISTRATION NUMBER: 31,071
 REFERENCE/DOCKET NUMBER: 3595-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5661 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..5661

US-08-938-105-2

Alignment Scores:
 Pred. No.: 326 GlnGlyHiSProSerThrGlyLeuIleThrProGlyProSerLeuSerGlnGly 345
 Score: 4.76e-08
 Percent Similarity: 175.00
 Best Local Similarity: 37.988
 Query Match: 22.92%
 DB: 4.49%
 Gaps: 19

US-09-837-602-2 (1-754) x US-08-938-105-2 (1-5661)

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 Db 2268 CAGGAGCGCTGCR--GGTATCCAGTGAACATCGGCCCTCATGGGGTCAAGAA 2324
 Qy 346 ValSerValAspGluLysLeuMet ProSer-AlaProValAsnThrThrTyrValAl 365
 Db 2325 TTGGCCGTCGATGAGCTCACTTCAGATCAAGATCAAGCTGAAGGAGCTGCTGAAGC-GC 2375
 Qy 365 aaspThrGluSerGluGlnAlaaspThrTyrPaspLeuSerGluArgProTyrS-- 382
 Db 2376 AGAGCAGAGGAAGGAGATGCCAACATGAAGGAGTTGGCGAGTCAGATGCACT 2435
 Qy 383 -----GluLysLeuValSerLysMetGluGlnLysPheArgMetLeuSerGlnAs 399
 Db 2436 AGAGAGTCAGGTCGGCCCAAGAGTCAGGAGAATGGAAAGTGGAAAGTCGCTGAGGA 2495

Qy 399 PalaProThrValLysGluSerCysLysThrSerAsnSerMetValSerAs 419
 Db 2496 GAGAAAGACCTCAGTCACAGTCAGGACAACTGAGCGGACAAAGACAAC- 2538
 Qy 419 nThrLeuIleAlaMetArgIleProAsnThrProThrLysLeuProSerII 439
 Db 2539 -----CTGATCAGTCAGAGAT 2585

Qy 439 eAsnLysSerLysBaspArgAlaSerGlnGlnGlnThrAsnSerLileArgAsnThrPhe 459
 Db 2541 GCGAGATGCCGAGGAGCCCTGCACACG- 2701

Qy 459 eGlnProSerThrLysBlysArg 476
 Db 2586 CCAGCTGGAGGCCAAGGTGAAGGAGATGACCGAGGTGGAGCAAGGAGATGAA 2645

Qy 476 r-----SerCysLysSerAlaArgIleGluThrSerCysSer--LeuLeuGluG 492
 Db 2646 CCCGAGCTACCGCAGAAGGCCAACCTGGAGACGAGTCAGCTGAGCTCAACAAAGA 2701

Qy 492 nThrGlnProAlaThrProSerLeuTyrLys--AsnLysGluGlnHisLeuSerGluG 511
 Db 2706 TATCGATGACCTGGAGGTGACCTGGCCDAGGTGAGGAAAGCAGGAAAGGAGAA 2766

Qy 511 nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerI 531
 Db 2766 CAAAG-----GTTAAAAACCT 2788

Qy 531 eValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuGluSerAsnLysLys- 550
 Db 2781 GACAGAGGAGATGCCGGCTGCGACAGAGATCATGCCAAGCTGACCAAGGAAACAAAGC 2844

Qy 551 -----ArgGluLysAspAspValAlaLeuGluAspGluValLeuGluG 564
 Db 2841 TCTTCAGANGGCCCAAGCCTAGTGTGCTTACGGCTGAGCTTACGGCTGAGGAGACAGCTGCAA 2900

Qy 564 uGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysValGlnLysGlnG 584
 Db 2901 CACACTG-----ACCAAGCTAAAGTCAGCTGGCAGAACCTGGAGCTGAGGAA 2954

Qy 584 uGluAspPheValAsnValAlaGluLysArgProArgMetAspIleGluThrAsnAspThrPhe 604
 Db 2952 GGGATCCCTGGAGCAGGAGCTGCATGGCAGCTGGAGCCAA 299

Qy 604 rAspGluAlaValProGluUserSerLysIleSerGlnGluLysGlyLysSer 624
 Db 2998 -----G-----G-----G-----G-----G-----G-----G-----G 3000

Qy 624 gGluLysGluAspSerLysSerAlaLysGluIleSerAsn-----AsnAspLys 642
 Db 3006 GAAGCTGAGGGTGAACCTGACCTGGAGGAGCATATGACACTTGAGAAGGACAA 3065

Qy 642 SerGluGlnAspSerGluMetLeuProLysIleLeuThrGluPheAspSerIle 662
 Db 3066 GCCTCAG-----CTGGAGGAAACCTCAAGAAAGAAGAGTT----- 3103

Qy 662 uValLysAsnSerThrSerArgAsnProSerGlyIleAsnBpAspTyrGly--G1 681
 Db 3103 -----GACATCAGTCAGCAGACAGCTAAATGAGGCGAGGAGGGCCCTGGC 3144

Qy 681 nleuLysAsnPheLysLysPheLysLysValThrTyrProGlyAlaGlyLysLeuProH1 701
 Db 3150 CCTCTAGTCGACAAGAAACTGAGGAA----- 3177

Qy 701 sIleIleGlySerAspLeuIleAlaLysIleAlaArgLysLeuIleGluGlnGly 721
 Db 3178 -----AACCAGGACRCGACATCGAGGAGTCGAGGA 3200

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Qy 741 Pasphephearg 745
 Db 3258 AGACCTGACCCGG 3270

RESULT 3
 US-08-923-992A-5
 Sequence 5, Application US/08923992A
 Patent No. 620738
 GENERAL INFORMATION:
 APPLICANT: Tai, Joseph Y.
 ADDRESS: Blake, Milian S.
 TITLE OF INVENTION: No. 620738-19A FC Binding Forms of the Group B
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sternin, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 ZIP: 20005
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923, 992A
 FILING DATE: 05-SEP-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/024, 707.
 FILING DATE: 06-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32, 893
 REFERENCE/DOCKET NUMBER: 1438-0140001/RWE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3384 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3384

US-08-923-992A-5
 Alignment Scores:
 PSeq. No.: 8.99e-08
 Score: 169.00
 Percent Similarity: 37.45%
 Best Local Similarity: 19.92%
 Query/Subject Match: 4.33%
 DB: 3

Length: 3384
 Matches: 142
 Conservative: 125
 Mismatches: 238
 Indels: 208
 Gaps: 38

Db 448 -----
 Db 490 CATTCAAAAGTCCTGGTAAAGCCAAAGGAATCACAAATGAGAT--- 546
 Db 547 -----AAGATTCTATGCTGAAAGAACAGCTCACAAAGCA 600
 Db 601 GATAAAAAGAAGATGCCGAACTTAAAGGTCTGAGAAGACTGGTAAACTCTTGTCTCA 660
 Qy 301 GlyLeuAlaValIlePhenMetThr 318
 Db 661 ACTAAAGCTGGCTGATCAAGAAATTATGAGATGTGAAGAACAGGT----- 714
 Qy 319 ThriySAsnTyrcysAspProGlyLeuLysProSerThrGlyLeuLysLeuMetProSerAlaProVal 358
 Db 715 -----AGTGAGGAAATAACTTCAGAAAGTGTGATGAACTAT-----GCT 753
 Qy 359 AsnThrThrTyrvAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuser 378
 Db 754 AAATGCCCTCAGAACCTGCTCAAATCTCTGAGAACTGATAAGGAACTACCAAT 813
 Qy 379 GluargProLysGluIleIleValSerIysMetGlu-----GlnLys----- 392
 Db 814 GAAACAGGTACACAGTTAAATCTCAATTCTGAGAAACGCTCAAAGGAACTACCAATG 873
 Qy 393 -----PheArgMetLeuSerGlnAspAlaPro 401
 Db 874 CAACTCTTATCAAGAACGAAATGTGAAATTSTAAGGCTATGAGTGAGAGCTGGAG 933
 Qy 402 ThrValLysGluSerCysLysThrSerAsnAsn-----SerMetValSerAsn 419
 Db 934 CAGCTTGAAAGGAAATTAAACATAATTGGAAAGCTATTAGAGATTTGTTGCGAAA 993
 Qy 420 ThreIleAlaLysMetArgIleProAsnTyrglnLeuSerProThrLys---IleProSer 438
 Db 994 TCTAAAGAAATCTGAGAAATACGAAAGAAACTATCAAAATCTTCAGAA 1053
 Qy 439 IleAsnLysSerLysAspArgAlaSerGln-----GlnGlnGlnThrAsnSerIleArg 456
 Db 1054 TTAAAGCAACTAGAGGAAAGTCATTCGAAACTTGAAACAGCTGGAGGTTTATAAGA 1113
 Qy 457 AsnTrPhe-----GlnProSerThrLysIleSArg---GluuArgAsp----- 469
 Db 1114 AAAAATTTAAACGTCAGGCAAGTACACCAAAACGTTGAAACGAGATTAGCT 1173
 Qy 470 -----GluGluAsnGlnGlnMetSerCysLysSerAlaArgIleGluThrSerCys 487
 Db 1174 GCTAAATGAAATAATCACAA-----AAGATGAGTAAACAGTT 1212
 Qy 488 SerLeuLeuGluGlnThrGlnProAlaThrProSerLeuIleGluGlnHis 507
 Db 1213 TCA-----CCAGAGATAATCACTGTATGAGGTGAAAGCTGGAA 1254
 Qy 508 LeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPheThrAsp---Thr 526
 Db 1255 TTTACA-----GTCACAGCTTAAGTGTGAAAGACGACTGGAACTTCAGT 1302
 Qy 527 AspLeuIysSerIleValLysAsnSerAlaSerLysSerHisAlaAaGluLysLeuArg 546
 Db 1303 GATCT-----TTAACAAAATAATCCTGTTGATCA-----GATAAAATGAT 1347
 Qy 547 SerAsnLysArgGluMetAspAspValAlaIleGluAspGluValLeuGluGlnLeu 566
 Db 1348 ACAAAATPATAAGACTAACACGATACTTCAGAAATCCTGAAACACTCA 447

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Qy 567 -----PhelYsAespthrLys-----Pro 572 ; APPLICANT: Xue, Aidong J.
 Db 1408 AAGCTTAATGCAAAGTCAAACAGTGAATCTAAACCTAAGATGATTCTGCAATGTAGT 1467 ; APPLICANT: Yang, Yonghong
 Qy 573 GluLeuGluLLeAspValLysValGlnLysGlnGluGluAspValAsnValArgLysArg 592 ; APPLICANT: Wang, Jian-Rui
 Db 1468 GAAAACATTCACTATTCAGTCAAAGAAAGGAGAAA---CAACGTCCTAAACAA 1524 ; APPLICANT: Zhou, Ping
 Qy 593 ProArgMetAspIleGluLhrAspThrPheserArgGluLavalProGluSerSer 612 ; APPLICANT: Ma, Yunging
 Db 1525 CCA-----GAGCAGAAAGATTCTAAACGGGAAAGGGTCTCTAGAACCA 1572 ; APPLICANT: Wang, Dunru
 Qy 613 LysIleSerGlnGluAsnGluIle-----GlyLysLysLysLysLysLysLys 627 ; APPLICANT: Wang, Zhiwei
 Db 1573 AAATCAAATGACAAGATCATTACAGGTGATAATTCACTGCTCAACAGAACCTGAA 1632 ; APPLICANT: John Tillinghast
 Qy 627 ----- 627 ; APPLICANT: Drmanac, Radivoje T.
 Db 1633 AAGTAGAAAAGCAATAAAAGAATTAAATGGAGAACCGAGATTCCATCCAATCCAG 1692 ; TITLE OF INVENTION: No. 65696261 Nucleic Acids and
 Qy 628 -----GluAspSerLeuIleTP-----SerAlaLysGlu-----IleSer 638 ; TITLE OF INVENTION: Polypeptides
 Db 1693 TATGGTATTCAAATCAATTGGAGTCACAAAAGGCTATCCGAAAGCCATAACAA 1752 ; FILE REFERENCE: 784 CIP2B
 Qy 639 AsnAsnAspLysLeuGlnAspAspSer----- 647 ; CURRENT APPLICATION NUMBER: US/09/620,312D
 Db 1753 AGTTAAAGAGATGATTGTTGATCATTCAAGGTGATAATTCAACAGGACTATTAAAC 1812 ; CURRENT FILING DATE: 2000-07-19
 Qy 648 -----GluMetLeuProYs 652 ; PRIORITY APPLICATION NUMBER: 09/552,317
 Db 1813 AAATATAATCTGATTATTGAAATTTCATGCAAAATGGAGATGCTGACTAGA 1872 ; PRIORITY FILING DATE: 2000-04-25
 Qy 653 LysLeuLeu-----ThrGluPheArgSerLeuValIle 664 ; PRIORITY APPLICATION NUMBER: 09/488,725
 Db 1873 AAATGGGTTCAAGGTCTAGTATATGACAAATATCTGATAATGCCAAATTAAAGG---ATATT 1929 ; PRIORITY FILING DATE: 2000-01-21
 Qy 665 LysAsnSerThrSerArgAsnProSerGlyIleAsnAspDAspPheGlyLysLysAsn 684 ; NUMBER OF SEQ ID NOS: 1105
 Db 1930 GAGTCAGATGATGAGAGAAAGAAA-----GAGATATTAGGGAAAGTTGAAATT 1980 ; SOFTWARE: pt_FL_genes Version 1.0
 Qy 686 -----PhelLysLysPhe----- 688 ; SEQ ID NO. 130
 Db 1981 GATGCTTCAAGGTCTATTGAAATTTCCTTACCACTTTAACCTAAATAAAATTAAAGCG 2040 ; LENGTH: 8503
 Qy 689 -----LysLysValThrTrpProGlyAlaGlyLysIleProHisIle 702 ; ALIGNMENT SCORES:
 Db 2041 ATGGTAGATGATTGATGAAAGTAAAGTAGACAAGATCAGCCAGCAAAATTCCGAA--- 2097 ; Pred. No.: 9.04e-07
 Qy 703 IleGlyGlySerAspLeuIleAlaHisIleAlaArgLysAsnThrGluLeuGluLysTrp 722 ; Score: 166.00
 Db 2098 -----AATCAGAAATGATCAGCTGCTTAAGGCTAAAGGCTAAAGTATGCTGTTATCAAGTAT 2151 ; Percent Similarity: 36.47%
 Qy 723 LeuArgGlnGluMetGluValGlnAsnGlnHis-----AlaLysGluLysSerLeuAla 740 ; Best Local Similarity: 20.09%
 Db 2152 ATGCTAAAGCTTTAGATCGAGTCATCACATCTGCAGAAAGAAATACTACAGTAAATT 2211 ; Mismatches: 282
 Qy 741 AspAspLeuAspPheArgTrpAsnProTrpLeuLysArgAsp 753 ; Indels: 265
 Db 2212 GTTGATCCTTTTAAAGAACCTTGAAGCGTAAACAA 2250 ; Gaps: 44
 Qy 747 ----- 747 ; LOCATION: (91)..(8082)
 Db 1690 US-09-837-602-2 (1-754) x US-09-620-312D-130 (1-8503) ; US-09-620-312D-130
 Qy 748 ----- 748 ; US-09-620-312D-130 (1-8503)
 Db 1729 GCGCGCTGAAACAGCAGAAAGATCACTTTGG----- 173 ; Length: 8503
 Qy 749 ----- 749 ; Matches: 173
 Db 1730 TGCCCAAGTTACTGGAAACTGACAATAATGTCATTATCAACTGTGGAACTTAATC 227 ; Conservativeness: 141
 Qy 750 ----- 750 ; Mismatches: 282
 Db 1731 CysAlaLleLeuIleGluAsn-AspGlnSerIle----- 751 ; Indels: 265
 Qy 751 ----- 751 ; Gaps: 44
 Db 1732 752 ; Length: 8503
 Qy 753 ----- 753 ; Matches: 173
 Db 1733 AGCGACCAATC 754 ; Conservativeness: 141
 Qy 754 ----- 754 ; Mismatches: 282
 Db 1734 CTICATTTGATGTTGCTCTTCATGGTATGAAACTACCAAAATGCTATGAAATAAT 755 ; Indels: 265
 Qy 755 ----- 755 ; Gaps: 44
 Db 1735 756 ; Length: 8503
 Qy 757 ----- 757 ; Matches: 173
 Db 1736 AGCGACCAATC 758 ; Conservativeness: 141
 Qy 759 ----- 759 ; Mismatches: 282
 Db 1737 760 ; Indels: 265
 Qy 761 pGluIleProValLeuThrLeuLysAspAsnSerLysTrpArgLeuIleThrGlyValValGlyArgLysAsn 81 ; Length: 8503
 Db 1738 AGCGACCAATC 761 ; Matches: 173
 Qy 762 ----- 762 ; Conservativeness: 141
 Db 1739 763 ; Mismatches: 282
 Qy 764 ----- 764 ; Indels: 265
 Db 1740 765 ; Gaps: 44
 Qy 766 ----- 766 ; Length: 8503
 Db 1741 767 ; Matches: 173
 Qy 768 ----- 768 ; Conservativeness: 141
 Db 1742 769 ; Mismatches: 282
 Qy 770 ----- 770 ; Indels: 265
 Db 1743 771 ; Gaps: 44
 Qy 772 ----- 772 ; Length: 8503
 Db 1744 773 ; Matches: 173
 Qy 774 ----- 774 ; Conservativeness: 141
 Db 1745 775 ; Mismatches: 282
 Qy 776 ----- 776 ; Indels: 265
 Db 1746 777 ; Gaps: 44
 Qy 778 ----- 778 ; Length: 8503
 Db 1747 779 ; Matches: 173
 Qy 780 ----- 780 ; Conservativeness: 141
 Db 1748 781 ; Mismatches: 282
 Qy 782 ----- 782 ; Indels: 265
 Db 1749 783 ; Gaps: 44
 Qy 784 ----- 784 ; Length: 8503
 Db 1750 785 ; Matches: 173
 Qy 786 ----- 786 ; Conservativeness: 141
 Db 1751 787 ; Mismatches: 282
 Qy 788 ----- 788 ; Indels: 265
 Db 1752 789 ; Gaps: 44
 Qy 790 ----- 790 ; Length: 8503
 Db 1753 791 ; Matches: 173
 Qy 792 ----- 792 ; Conservativeness: 141
 Db 1754 793 ; Mismatches: 282
 Qy 794 ----- 794 ; Indels: 265
 Db 1755 795 ; Gaps: 44
 Qy 796 ----- 796 ; Length: 8503
 Db 1756 797 ; Matches: 173
 Qy 798 ----- 798 ; Conservativeness: 141
 Db 1757 799 ; Mismatches: 282
 Qy 800 ----- 800 ; Indels: 265
 Db 1758 801 ; Gaps: 44
 Qy 802 ----- 802 ; Length: 8503
 Db 1759 803 ; Matches: 173
 Qy 804 ----- 804 ; Conservativeness: 141
 Db 1760 805 ; Mismatches: 282
 Qy 806 ----- 806 ; Indels: 265
 Db 1761 807 ; Gaps: 44
 Qy 808 ----- 808 ; Length: 8503
 Db 1762 809 ; Matches: 173
 Qy 810 ----- 810 ; Conservativeness: 141
 Db 1763 811 ; Mismatches: 282
 Qy 812 ----- 812 ; Indels: 265
 Db 1764 813 ; Gaps: 44
 Qy 814 ----- 814 ; Length: 8503
 Db 1765 815 ; Matches: 173
 Qy 816 ----- 816 ; Conservativeness: 141
 Db 1766 817 ; Mismatches: 282
 Qy 818 ----- 818 ; Indels: 265
 Db 1767 819 ; Gaps: 44
 Qy 820 ----- 820 ; Length: 8503
 Db 1768 821 ; Matches: 173
 Qy 822 ----- 822 ; Conservativeness: 141
 Db 1769 823 ; Mismatches: 282
 Qy 824 ----- 824 ; Indels: 265
 Db 1770 825 ; Gaps: 44
 Qy 826 ----- 826 ; Length: 8503
 Db 1771 827 ; Matches: 173
 Qy 828 ----- 828 ; Conservativeness: 141
 Db 1772 829 ; Mismatches: 282
 Qy 830 ----- 830 ; Indels: 265
 Db 1773 831 ; Gaps: 44
 Qy 832 ----- 832 ; Length: 8503
 Db 1774 833 ; Matches: 173
 Qy 834 ----- 834 ; Conservativeness: 141
 Db 1775 835 ; Mismatches: 282
 Qy 836 ----- 836 ; Indels: 265
 Db 1776 837 ; Gaps: 44
 Qy 838 ----- 838 ; Length: 8503
 Db 1777 839 ; Matches: 173
 Qy 840 ----- 840 ; Conservativeness: 141
 Db 1778 841 ; Mismatches: 282
 Qy 842 ----- 842 ; Indels: 265
 Db 1779 843 ; Gaps: 44
 Qy 844 ----- 844 ; Length: 8503
 Db 1780 845 ; Matches: 173
 Qy 846 ----- 846 ; Conservativeness: 141
 Db 1781 847 ; Mismatches: 282
 Qy 848 ----- 848 ; Indels: 265
 Db 1782 849 ; Gaps: 44
 Qy 850 ----- 850 ; Length: 8503
 Db 1783 851 ; Matches: 173
 Qy 852 ----- 852 ; Conservativeness: 141
 Db 1784 853 ; Mismatches: 282
 Qy 855 ----- 855 ; Indels: 265
 Db 1786 856 ; Gaps: 44
 Qy 857 ----- 857 ; Length: 8503
 Db 1787 858 ; Matches: 173
 Qy 859 ----- 859 ; Conservativeness: 141
 Db 1788 860 ; Mismatches: 282
 Qy 861 ----- 861 ; Indels: 265
 Db 1789 862 ; Gaps: 44
 Qy 863 ----- 863 ; Length: 8503
 Db 1790 864 ; Matches: 173
 Qy 865 ----- 865 ; Conservativeness: 141
 Db 1791 866 ; Mismatches: 282
 Qy 867 ----- 867 ; Indels: 265
 Db 1792 868 ; Gaps: 44
 Qy 869 ----- 869 ; Length: 8503
 Db 1793 870 ; Matches: 173
 Qy 871 ----- 871 ; Conservativeness: 141
 Db 1794 872 ; Mismatches: 282
 Qy 875 ----- 875 ; Indels: 265
 Db 1796 876 ; Gaps: 44
 Qy 877 ----- 877 ; Length: 8503
 Db 1797 878 ; Matches: 173
 Qy 879 ----- 879 ; Conservativeness: 141
 Db 1798 880 ; Mismatches: 282
 Qy 881 ----- 881 ; Indels: 265
 Db 1799 882 ; Gaps: 44
 Qy 883 ----- 883 ; Length: 8503
 Db 1800 884 ; Matches: 173
 Qy 885 ----- 885 ; Conservativeness: 141
 Db 1801 886 ; Mismatches: 282
 Qy 887 ----- 887 ; Indels: 265
 Db 1802 888 ; Gaps: 44
 Qy 889 ----- 889 ; Length: 8503
 Db 1803 890 ; Matches: 173
 Qy 891 ----- 891 ; Conservativeness: 141
 Db 1804 892 ; Mismatches: 282
 Qy 893 ----- 893 ; Indels: 265
 Db 1805 894 ; Gaps: 44
 Qy 895 ----- 895 ; Length: 8503
 Db 1806 896 ; Matches: 173
 Qy 897 ----- 897 ; Conservativeness: 141
 Db 1807 898 ; Mismatches: 282
 Qy 899 ----- 899 ; Indels: 265
 Db 1808 900 ; Gaps: 44
 Qy 901 ----- 901 ; Length: 8503
 Db 1809 902 ; Matches: 173
 Qy 903 ----- 903 ; Conservativeness: 141
 Db 1810 904 ; Mismatches: 282
 Qy 905 ----- 905 ; Indels: 265
 Db 1811 906 ; Gaps: 44
 Qy 907 ----- 907 ; Length: 8503
 Db 1812 908 ; Matches: 173
 Qy 909 ----- 909 ; Conservativeness: 141
 Db 1813 910 ; Mismatches: 282
 Qy 911 ----- 911 ; Indels: 265
 Db 1814 912 ; Gaps: 44
 Qy 913 ----- 913 ; Length: 8503
 Db 1815 914 ; Matches: 173
 Qy 916 ----- 916 ; Conservativeness: 141
 Db 1817 917 ; Mismatches: 282
 Qy 918 ----- 918 ; Indels: 265
 Db 1818 919 ; Gaps: 44
 Qy 920 ----- 920 ; Length: 8503
 Db 1819 921 ; Matches: 173
 Qy 922 ----- 922 ; Conservativeness: 141
 Db 1820 923 ; Mismatches: 282
 Qy 924 ----- 924 ; Indels: 265
 Db 1821 925 ; Gaps: 44
 Qy 926 ----- 926 ; Length: 8503
 Db 1822 927 ; Matches: 173
 Qy 928 ----- 928 ; Conservativeness: 141
 Db 1823 929 ; Mismatches: 282
 Qy 930 ----- 930 ; Indels: 265
 Db 1824 931 ; Gaps: 44
 Qy 932 ----- 932 ; Length: 8503
 Db 1825 933 ; Matches: 173
 Qy 934 ----- 934 ; Conservativeness: 141
 Db 1826 935 ; Mismatches: 282
 Qy 937 ----- 937 ; Indels: 265
 Db 1827 938 ; Gaps: 44
 Qy 939 ----- 939 ; Length: 8503
 Db 1828 940 ; Matches: 173
 Qy 941 ----- 941 ; Conservativeness: 141
 Db 1829 942 ; Mismatches: 282
 Qy 943 ----- 943 ; Indels: 265
 Db 1830 944 ; Gaps: 44
 Qy 945 ----- 945 ; Length: 8503
 Db 1831 946 ; Matches: 173
 Qy 947 ----- 947 ; Conservativeness: 141
 Db 1832 948 ; Mismatches: 282
 Qy 949 ----- 949 ; Indels: 265
 Db 1833 950 ; Gaps: 44
 Qy 951 ----- 951 ; Length: 8503
 Db 1834 952 ; Matches: 173
 Qy 953 ----- 953 ; Conservativeness: 141
 Db 1835 954 ; Mismatches: 282
 Qy 956 ----- 956 ; Indels: 265
 Db 1836 957 ; Gaps: 44
 Qy 958 ----- 958 ; Length: 8503
 Db 1837 959 ; Matches: 173
 Qy 960 ----- 960 ; Conservativeness: 141
 Db 1838 961 ; Mismatches: 282
 Qy 963 ----- 963 ; Indels: 265
 Db 1839 964 ; Gaps: 44
 Qy 965 ----- 965 ; Length: 8503
 Db 1840 966 ; Matches: 173
 Qy 967 ----- 967 ; Conservativeness: 141
 Db 1841 968 ; Mismatches: 282
 Qy 969 ----- 969 ; Indels: 265
 Db 1842 970 ; Gaps: 44
 Qy 971 ----- 971 ; Length: 8503
 Db 1843 972 ; Matches: 173
 Qy 973 ----- 973 ; Conservativeness: 141
 Db 1844 974 ; Mismatches: 282
 Qy 975 ----- 975 ; Indels: 265
 Db 1845 976 ; Gaps: 44
 Qy 977 ----- 977 ; Length: 8503
 Db 1846 978 ; Matches: 173
 Qy 979 ----- 979 ; Conservativeness: 141
 Db 1847 980 ; Mismatches: 282
 Qy 981 ----- 981 ; Indels: 265
 Db 1848 982 ; Gaps: 44
 Qy 983 ----- 983 ; Length: 8503
 Db 1849 984 ; Matches: 173
 Qy 985 ----- 985 ; Conservativeness: 141
 Db 1850 986 ; Mismatches: 282
 Qy 987 ----- 987 ; Indels: 265
 Db 1851 988 ; Gaps: 44
 Qy 989 ----- 989 ; Length: 8503
 Db 1852 990 ; Matches: 173
 Qy 991 ----- 991 ; Conservativeness: 141
 Db 1853 992 ; Mismatches: 282
 Qy 993 ----- 993 ; Indels: 265
 Db 1854 994 ; Gaps: 44
 Qy 995 ----- 995 ; Length: 8503
 Db 1855 996 ; Matches: 173
 Qy 997 ----- 997 ; Conservativeness: 141
 Db 1856 998 ; Mismatches: 282
 Qy 999 ----- 999 ; Indels: 265
 Db 1857 1000 ; Gaps: 44
 Qy 1001 ----- 1001 ; Length: 8503
 Db 1858 1002 ; Matches: 173
 Qy 1003 ----- 1003 ; Conservativeness: 141
 Db 1859 1004 ; Mismatches: 282
 Qy 1005 ----- 1005 ; Indels: 265
 Db 1860 1006 ; Gaps: 44
 Qy 1007 ----- 1007 ; Length: 8503
 Db 1861 1008 ; Matches: 173
 Qy 1009 ----- 1009 ; Conservativeness: 141
 Db 1862 1010 ; Mismatches: 282
 Qy 1011 ----- 1011 ; Indels: 265
 Db 1863 1012 ; Gaps: 44
 Qy 1013 ----- 1013 ; Length: 8503
 Db 1864 1014 ; Matches: 173
 Qy 1015 ----- 1015 ; Conservativeness: 141
 Db 1865 1016 ; Mismatches: 282
 Qy 1017 ----- 1017 ; Indels: 265
 Db 1866 1018 ; Gaps: 44
 Qy 1019 ----- 1019 ; Length: 8503
 Db 1867 1020 ; Matches: 173
 Qy 1021 ----- 1021 ; Conservativeness: 141
 Db 1868 1022 ; Mismatches: 282
 Qy 1023 ----- 1023 ; Indels: 265
 Db 1869 1024 ; Gaps: 44
 Qy 1025 ----- 1025 ; Length: 8503
 Db 1870 1026 ; Matches: 173
 Qy 1027 ----- 1027 ; Conservativeness: 141
 Db 1871 1028 ; Mismatches: 282
 Qy 1029 ----- 1029 ; Indels: 265
 Db 1872 1030 ; Gaps: 44
 Qy 1031 ----- 1031 ; Length: 8503
 Db 1873 1032 ; Matches: 173
 Qy 1034 ----- 1034 ; Conservativeness: 141
 Db 1874 1035 ; Mismatches: 282
 Qy 1036 ----- 1036 ; Indels: 265
 Db 1875 1037 ; Gaps: 44
 Qy 1038 ----- 1038 ; Length: 8503
 Db 1876 1039 ; Matches: 173
 Qy 1040 ----- 1040 ; Conservativeness: 141
 Db 1877 1041 ; Mismatches: 282
 Qy 1042 ----- 1042 ; Indels: 265
 Db 1878 1043 ; Gaps: 44
 Qy 1044 ----- 1044 ; Length: 8503
 Db 1879 1045 ; Matches: 173
 Qy 1046 ----- 1046 ; Conservativeness: 141
 Db 1880 1047 ; Mismatches: 282
 Qy 1048 ----- 1048 ; Indels: 265
 Db 1881 1049 ; Gaps: 44
 Qy 1050 ----- 1050 ; Length: 8503
 Db 1882 1051 ; Matches: 173
 Qy 1052 ----- 1052 ; Conservativeness: 141
 Db 1883 1053 ; Mismatches: 282
 Qy 1054 ----- 1054 ; Indels: 265
 Db 1884 1055 ; Gaps: 44
 Qy 1056 ----- 1056 ; Length: 8503
 Db 1885 1057 ; Matches: 173
 Qy 1058 ----- 1058 ; Conservativeness: 141
 Db 1886 1059 ; Mismatches: 282
 Qy 1060 ----- 1060 ; Indels: 265
 Db 1887 1061 ; Gaps: 44
 Qy 1062 ----- 1062 ; Length: 8503
 Db 1888 1063 ; Matches: 173
 Qy 1064 ----- 1064 ; Conservativeness: 141
 Db 1889 1065 ; Mismatches: 282
 Qy 1066 ----- 1066 ; Indels: 265
 Db 1890 1067 ; Gaps: 44
 Qy 1068 ----- 1068 ; Length: 8503
 Db 1891 1069 ; Matches: 173
 Qy 1070 ----- 1070 ; Conservativeness: 141
 Db 1892 1071 ; Mismatches: 282
 Qy 1073 ----- 1073 ; Indels: 265
 Db 1893 1074 ; Gaps: 44
 Qy 1076 ----- 1076 ; Length: 8503
 Db 1894 1077 ; Matches: 173
 Qy 1078 ----- 1078 ; Conservativeness: 141
 Db 1895 1079 ; Mismatches: 282
 Qy 1080 ----- 1080 ; Indels: 265
 Db 1896 1081 ; Gaps: 44
 Qy 1082 ----- 1082 ; Length: 8503
 Db 1897 1083 ; Matches: 173
 Qy 1084 ----- 1084 ; Conservativeness: 141
 Db 1898 1085 ; Mismatches: 282
 Qy 1086 ----- 1086 ; Indels: 265
 Db 1899 1087 ; Gaps: 44
 Qy 1090 ----- 1090 ; Length: 8503
 Db 1900 1091 ; Matches: 173
 Qy 1092 ----- 1092 ; Conservativeness: 141
 Db 1901 1093 ; Mismatches: 282
 Qy 1094 ----- 1094 ; Indels: 265
 Db 1902 1095 ; Gaps: 44
 Qy 1096 ----- 1096 ; Length: 8503
 Db 1903 1097 ; Matches: 173
 Qy 1098 ----- 1098 ; Conservativeness: 141
 Db 1904 1099 ; Mismatches: 282
 Qy 1100 ----- 1100 ; Indels: 265
 Db 1905 1101 ; Gaps: 44
 Qy 1102 ----- 1102 ; Length: 8503
 Db 1906 1103 ; Matches: 173
 Qy 1104 ----- 1104 ; Conservativeness: 141
 Db 1907 1105 ; Mismatches: 282
 Qy 1108 ----- 1108 ; Indels: 265
 Db 1909 1109 ; Gaps: 44
 Qy 1110 ----- 1110 ; Length: 8503
 Db 1911 1111 ; Matches: 173
 Qy 1112 ----- 1112 ; Conservativeness: 141
 Db 1913 1113 ; Mismatches: 282
 Qy 1114 ----- 1114 ; Indels: 265
 Db 1915 1115 ; Gaps: 44
 Qy 1116 ----- 1116 ; Length: 8503
 Db 1917 1117 ; Matches: 173
 Qy 1118 ----- 1118 ; Conservativeness: 141
 Db 1918 1119 ; Mismatches: 282
 Qy 1120 ----- 1120 ; Indels: 265
 Db 1919 1121 ; Gaps: 44
 Qy 1122 ----- 1122 ; Length: 8503
 Db 1920 1123 ; Matches: 173
 Qy 1124 ----- 1124 ; Conservativeness: 141
 Db 1921 1125 ; Mismatches: 282
 Qy 1126 ----- 1126 ; Indels: 265
 Db 1927 1127 ; Gaps: 44
 Qy 1128 ----- 1128 ; Length: 8503
 Db 1929 1129 ; Matches: 173
 Qy 1130 ----- 1130 ; Conservativeness: 141
 Db 1931 1131 ; Mismatches: 282
 Qy 1132 ----- 1132 ; Indels: 265
 Db 1933 1133 ; Gaps: 44
 Qy 1134 ----- 1134 ; Length: 8503
 Db 1935 1135 ; Matches: 173
 Qy 1136 ----- 1136 ; Conservativeness: 141
 Db 1937 1137 ; Mismatches: 282
 Qy 1138 ----- 1138 ; Indels: 265
 Db 1939 1139 ; Gaps: 44
 Qy 1140 ----- 1140 ; Length: 8503
 Db 1940 1141 ; Matches: 173
 Qy 1142 ----- 1142 ; Conservativeness: 141
 Db 1941 1143 ; Mismatches: 282
 Qy 1144 ----- 1144 ; Indels: 265
 Db 1945 1145 ; Gaps: 44
 Qy 1146 ----- 1146 ; Length: 8503
 Db 1947 1147 ; Matches: 173
 Qy 1148 ----- 1148 ; Conservativeness: 141
 Db 1949 1149 ; Mismatches: 282
 Qy 1150 ----- 1150 ; Indels: 265
 Db 1951 1151 ; Gaps: 44
 Qy 1152 ----- 1152 ; Length: 8503
 Db 1953 1153 ; Matches: 173
 Qy 1154 ----- 1154 ; Conservativeness: 141
 Db 1955 1155 ; Mismatches: 282
 Qy 1156 ----- 1156 ; Indels: 265
 Db 1957 1157 ; Gaps: 44
 Qy 1158 ----- 1158 ; Length: 8503
 Db 1959 1159 ; Matches: 173
 Qy 1160 ----- 1160 ; Conservativeness: 141
 Db 1961 1161 ; Mismatches: 282
 Qy 1162 ----- 1162 ; Indels: 265
 Db 1963 1163 ; Gaps: 44
 Qy 1164 ----- 1164 ; Length: 8503
 Db 1965 1165 ; Matches: 173
 Qy 1166 ----- 1166 ; Conservativeness: 141
 Db 1967 1167 ; Mismatches: 282
 Qy 1168 ----- 1168 ; Indels: 265
 Db 1969 1169 ; Gaps: 44
 Qy 1170 ----- 1170 ; Length: 8503
 Db 1971 1171 ; Matches: 173
 Qy 1172 ----- 1172 ; Conservativeness: 141
 Db 1973 1173 ; Mismatches: 282
 Qy 1174 ----- 1174 ; Indels: 265
 Db 1975 1175 ; Gaps: 44
 Qy 1176 ----- 1176 ; Length: 8503
 Db 1977 1177 ; Matches: 173
 Qy 1178 ----- 1178 ; Conservativeness: 141
 Db 1979 1179 ; Mismatches: 282
 Qy 1180 ----- 1180 ; Indels: 265
 Db 1981 1181 ; Gaps: 44

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Db	489	AATACAAATGAAACCATTACAGATTACTCTGGCACTCAAAATGAAACCTTTAT	548	Qy	471	uAsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuG1	491
Qy	176	rPheThrGluPheLeuLysAlaValGlnSerLysGlnProGlnIleGluSerPhe 196		Db	1482	TGTCCTGTTAGAGCTGATGTTTCAGTAACTCTGATACTTAACTGAGATA	1536
Db	549	TATTCGAGAGATGCAATAGG-----AATGTRGTA	578	Qy	491	uGlnThrGlnProAlaThrProSerLeuTrpLysAsnGlnHisLeuSerGluLys 511	
Qy	196	eTyrProProIleAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArgG1	216	Db	1537	-GATGGAAATCCACCAAAAGCTACTA-----ATCAGGACRATAAGAAATGAGTT	1589
Db	579	TGTGGCTGATCACAGAAGAGTCTATACATCAGAAATGGCTTG-----	627	Qy	511	nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerI1	531
Qy	216	nGluArgLysClnIlePheLysGly---LysThrPheIleLeuAsnAlaLysGlnHi	235	Db	1590	GAACCTACATCTCGTCTGACTATGATACTGTTAATCTGTTAATCTGAGACAGA	1649
Db	628	-----AAATGGATTACAAAGGGGAAATGAGCCATTATGGAGAACAAAATGAA	680	Qy	531	evallysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysSer 551	
Qy	235	glyLysSerLeuSer---SerAlaValValPheGlyIgylGluAlaArgIleIleThrG1	254	Db	1650	AAARAAAATG-----	
Db	681	TCAAGAAGGAGTCGTTCTCATACCTTT-----AGATGATTGGA	725	Qy	551	-GATGAAATTAAAAGAAAAGAA	1685
Qy	254	uGluAsnGluCgIgIgIuHiBsnPheLeuAlaProGlyThrCys-----	269	Db	1686	TGATTGGAT-----	
Db	726	AAGCAGAGAGGGTGA-----cctCTTAATTGTGAGGATCTGTTA	770	Qy	571	sProGluLeuGluIleAspValAlaIleGluAspGluValLeuLysGlnLeuPheLysAspThrLys 591	
Qy	270	-----ValValAsp-----	275	Db	1734	A-----CAGATGCAACTAACTCATGAAATTTCGAACTTAAGGATTAAGGATCGAGA	1790
Db	771	GGTATCCATTGAAATTGGTGTATCTGGCTGGCCAGTGTGCTCAAAGGCC	830	Qy	591	SArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaValProGluE 611	
Qy	275	ethRhsnSerGlnThrLeuIleProAspCysGlnLysIleTrpIleGlnSerIleMetA8	295	Db	1791	AGATATAATCAGATCTT-----	
Db	831	TGCAGCTGTCGGG---CTCAAGGAGGCATAAT-----ATAATCGAACCTTAT	878	Qy	611	rSerLysIleSerGlnGluAsnGluIleGlyLysSerArgGluLeu-----LyG1	628
Qy	295	pMetLeuGlnArgGlnGlyLeuIleProGluAlaGluIleGlyLeuAlaValI1	315	Db	1810	-----	
Db	879	TATTTG---GGCAAGTGTGATCAAAACCTAGGACAAGTGGGGTTICATA-----	933	Qy	628	uAspSerLeuTrpSerAlaLysLysIleSerAsnAsnAspLysLeuGlnAsp-----645	
Qy	315	ePheMetThr-ThrIleAsnTyrCysAspProGln-----	326	Db	1854	AGACCGATTAAGAGCTACAGGAAATCATGACTCTCAAACCTGAAATAAAAT	1913
Db	934	-----AATTATCGGATACCAAGGTTAACAGCAATTCTCAGAAATTCCCT	977	Qy	646	-----	
Qy	327	---GlyHisProSerThrGly---LeuIleThrThrProGlyProSerLeuSerI1	344	Db	1914	GGACTTGTCATACTCATGGAAGCATGAAAGCAGCCAAACAAATGAGCAGCTCTGTT	1973
Db	978	GGGAGGAATTCGAAAGACAGCTATTGCACTATTCTCCA-----	1020	Qy	659	eArgSerIleValIleLysSerAsnSerThrSerArgAsnProSerGlyIleLeuAsnAspA9P-----678	
Qy	344	glyValSerValAspGluIleLeuMetProSerAlaProValAsnThr-----	360	Db	1974	TGATGTCGAAACTGTGCCCTGATGCCAAGAGAAATCAGCCTTCATGAAATGAA	2033
Db	1021	---GTATCTTTGATGAACCTCTACTGCTCTCAGTGAACGTTGCTAAATATA1076		Qy	679	-----	
Qy	361	-----ThrThrIleValAlaAspThrGluSerGlnAla-----	372	Db	2034	TCTGGAGITGAAGGAGAAATGAAAGACTTGCAAACTTACAGGAAATGAA	2093
Db	1077	GAAGATACTCTATGTAATGAGGTATACTGAGCTCTCCTAAAGGTATAG	1136	Qy	684	-----	
Qy	373	---AspThrIleProIleSerGluIleArgProLysGluIleValSerLysMetGlnG1	391	Db	2094	TAFTCACTGTTATCAAACCAATTGGAGCAAAAGAGAAAATCAGTGTGAGAA	2153
Db	1137	AAAAAAATTAATGGATCTAAACAACTAGGAGGT-----TCCTTGTAGAAC	1187	Qy	685	-----	
Qy	391	nLysPheArgMetLeuSerGlnAsp-----AlaProThrValLysGluSerCysLysThr 409		Db	2154	AGATAATCAATCTGCTTTAATGAGATAACAAACTCACCTCCCTATAGATGCAAGT	2213
Db	1188	GCGGCTCTGGCAATGGGAAATGCAACTTGGCCAAACTTGGAGAAAGATGCT 1247		Qy	699	uProHisIleGlyGlySerAspLeuIleAlaHis-----HisAlaArgLysSerI1	717
Qy	409	rSerSerAsnAsnSerMetValSerAsnThrLeuIleAspGlnAspAsnLysMetArgIleProAsnI1	429	Db	2214	TCCA-----AAATGTTGCTCTGTAATGTTGGATTGGAAAGGAAAGATTAC	2258
Db	1248	TCAGAAAGTAGCAGATGAGAACAAATGAAAC-----TTAACACGGATGCTGTC	1304	Qy	717	rGluLeuGluIleTrpIleArgGlnGluMetGluValGlnAsnGlnHisAlaLysGlnG1	737
Qy	429	rGlnIleSerProProIleS-----	Le 436	Db	2259	TGATCTTCAGAAAGAAGCTTGTGCTT-----	
Db	1305	TTCCCTCACTGCAACAGGAAATTAAGCTAAAGGCTAAACTTGGCT 1364		Qy	737	u 737	
Qy	436	uProSerIleAsnLysSerLysAspDargIleSerGlnGlnGlnIleThrAsnSerIleAsn 456		Db	2316	A 2316	
Db	1365	TGGCAAAATTAACAACTGAAAC-----TCAAACTATGGAGATCAATTTAAATACCAAC	1421	RESULT 5			
Qy	456	gAsnTyrPheGlnProSerThrIys-----LyArgGluArgAspGluG1	471	US-09-043-597-119			
Db	1422	AAATAAACAAACACATAAGCTTCTATAATTATTACGAGAATTGATGATC 1481		Sequence 119, Application US/09643597			
				Patent No. 6426072			

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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel K.
APPLICANT: Wang, Ajun
APPLICANT: Skeky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeil, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-455C11

CURRENT APPLICATION NUMBER: US-09-643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 119
LENGTH: 8948
TYPE: DNA
ORGANISM: Homo sapien
US-09-643,597-119

Alignment Scores:

Pre. No.:	1.44e-06	Length:	8948
Score:	164.50	Matches:	187
Percent Similarity:	34.23%	Conservative:	132
Best Local Similarity:	20.06%	Mismatches:	295
Query Match:	4.22%	Indels:	319
DB:	4	Gaps:	45

US-09-837-602-2 (1-754) x US-09-643-597-119 (1-8948)

Qy 2 TrpLeuProAlaAlaGlyProAlaGlyGlyGluProTyroArgLeuLeuThrGly 21
Db 23301 TGGATGCTGATG-----

Qy 22 ValGluTyrrValGlyArgLysAsnCysAlaLeuLeuGluAsnAspGinSerile 41
Db 2367 ATAGGCCACCTGGGGCAGGATGACTCTCAAAACCTCCCTCTAGAACCGGG---- 2423

Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheserValThrAsnLeuSerGin 59
Db 2424 TCTTCTCACCATCACAGTCAAAATTAACTAGAGCTTAAGAGTCAGATGATTCAAA 2433

Qy 60 ThrAspGluLysProValLeuThrLeuLysAspAsnSerLysThrGlyThrPheValAla 79
Db 2484 GCAATGCTGAGGTCTCAACCGCTTAAGAT-----ATGCTTGCCAACTTCAGAGGT 2537

Qy 80 GluGluLys-----MetGlnLys-----GlyPheSerArgThrLeuLysSer 93
Db 2538 TCTGAAGATGATCTGTTATACAGATGAGTATTGGAAGCTTCAAGAAAT 2597

Qy 94 GlyAspGlyLleThrPheGlyValPheGlyValSerLysPheArgLleGluTyrrGluProLeu 113
Db 2598 ATCAATGGTGTACAGATGGTACTTAAATGCTTAAATGCTTAAATGCTTAAAT 2645

Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaLeu 133
Db 2646 -----

Qy 134 GlnLeuGlyLysPheThrValAsnSerThrGlyLysThrHisLeuValMetVal 153
Db 2667 CAA-----

Qy 154 SerValLeuValThr-----IleLysThrIleCys-----AlaLeu 165
Db 2694 GAAGGCCAGGGCTCACTGGAGGAAACTGTCTGCCCTGGATAAAGTGGAAAGCTTAC 2753

Qy 166 IleCysGlyLysArgProIleValValSerProGlu-----

Db 2754 CGCTGTGGACTGTGAAGAAAATAAAAATGACTTGAACTTGAACTTGCTGTTGTTGCCACT 2813
Qy 176 TyrPheThrGluPheLeuDysAlaValGinSerIleSlyGlnProProGlnIleGluUser 195
Db 2814 ATGAGACGAACTACAGAAAGCCGAGGATCCACTCTAGACTTCACGAGTATCCA 2873
Qy 196 PheTyrProProLeuAspGluProSerIleGlySerIleSasnValAspLeuSerGlyArg 215
Db 2874 CTTAT-----GATCAGCTGGAAAGTGGTGAAGAAAGTCACACGTCACAGCTGACAGACCGC 2930
Qy 216 GlnGluIarg-----LysGlnIlePhe 222
Db 2931 TGGCAAGGATAGATAAAACAGATCGACTTATGGGACCTGAGAAACATATCAAG 2990
Qy 223 LysGlyLysThrPhe-----IlePheLeuAsnAla 232
Db 2991 CAATGAGGAATTTATCGTATAACTATCAGGCTTCTGCAAGTGGCTPATGATGCTAAA 3050
Qy 233 LysGlnHisIleSlySLeuSerSerAlaValPheGlyLysGluIaArgLeuIle 3052
Db 3051 CGCCCCAGGATTCTTGAATCCGAAATCTGAATTT-----GGAGATTCACACAGTC 3101
Qy 253 ThrgluGluAsnGluGluLysIleAsnSphPheLeuAlaProGlyThrCysValValAsp 272
Db 3102 ATGCCGTTTTGAAATGAGCAAGAACACTG-----

Db 3132 -----

Qy 273 ThrglyIleThrAsnSerGlnIleThrLeuIleProAspCysGlnIlySlysTrpIleGlnSer 292
Db 3228 GCC-----

Qy 3132 -----

Db 3228 GGC-----

Qy 3293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProGluAlaGluIleGlyLeu 312
Db 3180 ATTGTGAACCTTGCCAAATTCA-----ATTAAGGATATGAGCTCAAGTGT 3227

Qy 3313 AlaValIlePheMetThrThrLysAsnTyrcysAspProGlnGlyHisProSerThrGly 332
Db 3328 GGC-----

Qy 333 LeuIysThrThrProGlyPro-----SerLeuSerGlnIleYval 346
Db 3246 CTGGAACACTGTGTCGAAACATACCTTCAGAGGAAOCATGATTCAAGGGACATGCTCGGTACATGAACTTAC 3305
Qy 3447 SerValAspIleLysLeuMetProSerAlaProValAsnThrThrIleIleGly 346
Db 3306 ATTGCGAAGAGGC-----TGCAAGATGTTCACTCGTCAATGAACTAC 3355
Qy 367 ThrgluUserGluGlnIalaAspThr-Tyr-Pro-Asp-----LeuSerGluArgProly 382
Db 3356 -----

Qy 382 GluIleLysValSerLysLeuMetProSerAlaProValAsnAsnSer-MetValSerAsnThrIleIleGly 3397
Db 3398 GAGTTGGAGATCTGAACTGAAATAACCAAGATGAGTTGGAGGAGGCTCTAG 3457
Qy 401 othrVallySleGluSerCysLysThrSerSerAsnAsnSer-MetValSerAsnThrIleIleGly 421
Db 3458 ACTGCCGAGATGCCAACTGGAAACIGTAATAAGACAAATTCTGATCAGAACCT 3517
Qy 421 uAlaIysMetArgIleProAsnTyrglnIleUserProThrIlyIleUserProSerIleAsnLys 441
Db 3518 GCAGGAAATACCGGAGAGTGTCCAGTCTCAA-----GCGAAGCTGCTGAGGA 3574
Qy 441 SerIleSasPargAla-----

Db 3575 GCTGAGAGACGGCTGAGCTGGATGGAGCTGGTAACTGAGCAAGTGCTA 3634
Qy 447 -----

Db 3635 CGGCCAAATAAAAGAACTCATGAGAAGATCACCGGACTGACTTGAGATTGAGATGA 3694
Qy 448 nGlnGlnGlnThrAsnSerIleArgAsnTyrrPhe-----

Db 3695 AAAGGGAAGAGAAAATCTGGAAGACAGATTGACCAACAGAAATGACTATGACCA 3754

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Qy	166 IleCysGlyArgProlleVallysProGlu-----	175	Db	3695 AAAGGAGAGAGAAAATCTGGAAGAACAGATTGACCAACAGAAATGACTATGACCA 3754
Db	2754 CGCTGTGAACTGAGAAATAAAATGACTGAACTTGAAGAAGCTGGTTGGCAACT 2813	459	Qy	176 TyrPheThrGluPheLeuIysAlaValGlnSerIysLysGlnProGlnIleGluSer 195
Db	2814 ATGAAAGACAGAACTACAGAAAGCCAGCATCCACTCTAGACTTCACAGCAGATCCA 2873	460	Db	3755 ACTGGAGAAAGCAAGGCAATGTGAAAGAGAACCTTGGTTGGCAAAATTAGAGTCAG 3814
Qy	196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArg 215	461	Qy	3815 GAAACCCATCAAGGAGAAGGAGTACGAGATTGAAAGGTTGAGGETTCATGAGCAAGA 3874
Db	2874 CTTTAT---GATCTGAACTTGGCAAGTTCGTTGAAAGACTCACACGTCAGACCCG 2930	462	Db	3875 AGGCCCCGGAGAGAGAAATGAAATGAGCTGGCAAAAGGTAAAGAAACCACTATATGA 3934
Qy	216 GluGluArg-----LysGlnIlePhe 222	463	Db	3875 AGGCCCCGGAGAGAGAAATGAAATGAGCTGGCAAAAGGTAAAGAAACCACTATATGA 3934
Db	2931 TGGCAAGGATAGATAAACAGATCGACTTGAATGAGTTGAGATTGAGCTGGAGAACATACAG 2990	464	Qy	3875 nGluMetSerCysLysSerAlaArgIleGluThrSerCysLeuLeuGluGlnThr 493
Qy	223 LysGlyLysThrPhe-----IlePheLeuAsnAla 232	465	Db	3935 GGAGTGAGTAATTAGGAAAC 4046
Db	2991 CAATTCAGGAAATTATGCTGATAACTATCAGCTTCTGCAAGTGCCTPATGTCATAA 3050	466	Qy	461 oSerThrLysBsrGluIargAspGlu-----AsnGln 473
Qy	233 LysGlnHisLysLysLeuSerSerAlaValValPheGlyGlyYgluAlaArgLeuIle 252	467	Db	3935 GAAACCCATCAAGGAGAAGGAGTACGAGATTGAAAGGTTGAGATTACAGAGACAC 3991
Db	3051 CGCCGCAGGATTCCCTTAAGATCCATGAAATT-----GGAGATTCACACAGTC 3101	468	Qy	461 oSerThrLysBsrAspAsnAlnLeuPheThrAspLys-----SerIleVa 532
Qy	253 ThrGluGluLysGluGluIuhiAsnProPheLeuAlaProGlyThrCysValValAsp 272	469	Db	4047 -CTTGATAGACTTCAAGGGTAAATTGTT 4093
Db	3102 ATGGCGTTTTGAAATGAGCAGAGACTG-----	470	Qy	532 LysAsnSerAlaSerAlaSerAlaLysLeuIargSerAsnLysSerArgGly 552
Qy	273 ThrGlyIleThrRhsSerGlnThrLeuIleProAspCysGlnIlysLeuIlePheIleSer 292	471	Db	4094 CAGGGTCAAATGACACCATCTTGCAAGGCCACTGAGGCAAGGCTGAAGAAACGC 4153
Db	3132 -----CACAGTGAATAATGTCGAAACGACAATCGAGGAGATGAAAAA 3179	472	Qy	513 oValAspPheThrAsnSerAspAsnAlnLeuPheThrAspLys-----SerIleVa 532
Qy	293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProlleProGluAlaGluIleGlyLeu 312	473	Db	4094 CAGGGTCAAATGACACCATCTTGCAAGGCCACTGAGGCAAGGCTGAAGAAACGC 4153
Db	3180 ATTGGCTGAACUTTGGCCAAATTCA-----ATTAAAGGATTATGAGCTCCAGCTG 3227	474	Qy	552 uMetAspAspPheValAlaGluAspGluValleuLeuGluGlnLeuPheLysAspThrLysSpr 572
Qy	313 AlavallePheMetThrThrLysBsrIuhiAspProGlnGlyHiisProSerThrGly 332	475	Db	4154 CCTTGAGCAAAGGCCCTGTCGGCTGAGATAATGAGAC 4198
Db	3228 GCC-----TCATAC-----ACCTCAGGA 3245	476	Qy	572 oGluLeuGluIleAspValLys-----ValGlnLysGluGluAspValAsnValArgLys 591
Qy	333 LeuIysThrThrThrProGlyPro-----SerIleSerGlnGlyVal 346	477	Db	4199 GCATCTGGAGATAACTGAGCAGTCATGCAAGGCTCTGAGGACATGCCC GGCA 4258
Db	3246 CTGGAAACTCTGCTGAACTACATCAAGGGACCATGATTCAAGGGACCATGCTCCCTCTGGGTG 3305	478	Qy	591 sArgIleArgMetAspIleGluIleThrAsnAspThr-----
Qy	347 SerValAspGluIleLeuMetProSerAlaProValAsnThrThrThrProValAlaAsp 366	479	Db	4259 CAAGGAGTCCTGGGG-----GAGGCTGCCAGACCATTCAGACAAAATAAGGAGATCTGA 4315
Db	3306 ATTCTGCAAGGGCC-TGCGAGATGTCATGAGTCATGAACTGAACTACTAC-----	480	Qy	603 -----PheSerAspGluAlaValProGluSerSerIleSerGlnGly 617
Qy	367 ThrGluSerGlnIalaAspThrItrp-Asp-----LeuSerGluArgProly 382	481	Db	4316 GAGACTCAAGGTGAGTTTCAGGAGGGCC-----AAGCCCGCTGGGAAATATGA 4366
Db	3356 -----AAGATCTGGAGGAACTTACAGGTTCTTAAGTGAAGTGCAG 3397	482	Qy	617 uAsnGluIleGlyLysBsrArgGluLeuIysGluAspSerLeuTrpSerAlaLys-----
Qy	382 sGluIleLysValSerIlysMetGluGln-----LysPheArgMetLeuSerGlnAspAlaP 401	483	Db	4367 AAATGAACTGAGTAAAGGATTAAGGAGATTAAGGAGCT 4426
Db	3398 GAGTTGGAAAGATCTGAACTGAAATAACGCTTAAGTGAAGTGTGAAAGGAGCTCAG 3457	484	Db	635 -----
Qy	401 othrValIlysGluSerCysLysThrSerSerAsnAsnSerMetValAsnSerAsnThrLe 421	485	Qy	4427 GTTGAGCCGAGATGCCAACTGGAAACTCTGGTAATAGAACAAATTCGTTGGCAAGT 4486
Qy	3458 ACTGGCCGAGATGCCAACTGGAAACTCTGGTAATAGAACAAATTCGTTGGCAAGT 3517	486	Db	636 -GluIleSerAsnAsnAspLysLeuGluMetLeuProLysLysLeuLeu 655
Qy	421 uAlaIysMetArgIleProLysIleProIleProIleProIleAsnLys 441	487	Db	4487 AGGAGATAACGGTGCCTACGGGCTCAGATAGAACATCTACCCGAGAAAACGAGCT 4546
Db	3518 GCAGAAATACAGGCCAGGAGTGGCTCCAGTCAA-----GCCAGAGTGGCTGGCTGGAGA 3574	488	Qy	655 uLeuThrGluPheArgSerIleValIleBsrSer-----ThrSerArgAsnPr 672
Qy	441 sAspIysAspArgAla-----	489	Db	4547 ATCTGAAAGATAAAAGGCTG-----AGAACACTCTAACCCGAGAACATCT 4600
Db	3575 GCTGAAGAGACAGGCTGAGCTGGATCGGAAGTCCAGAAATCTAGACAAGTCGCTA 3634	490	Qy	672 oSerIleIleAsnAspAspIysGlyIleLeuIysLeuIysSerIleAsnIleAsnIle 692
Qy	447 -----	491	Db	4601 CAGGGGGCTGAAAGAGACATCCACAG-----CAAAAGGCCAC 4639
Qy	3635 CGGCCAAATAAAAGAACTCAATGAGAAAGATCACCCGACTGACTTATGAGATTGAGATGA 3694	492	Qy	692 rTyrProGlyAlaGlyIleLeuProHisIleIleGlyGlySerAspLeuIleAlaIshishi 712
Qy	448 nGlnGlnGlnIhrAsnSerIleArgAsnItrPhe-----	493	Db	4640 T-----GGCTCTGGGTG-----GlutMetGluValGln 4652
Db	449 nGlnGlnGlnIhrAsnSerIleArgAsnItrPhe-----	494	Qy	712 sAlaArgLysAsnThrGluLeuGluItrpLeuIargGln-----GlutMetGluValGln 730

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Db	4653	-TCTAGAGGAAACAGGAGCTGGAGGTAGCTAGACAGTCAGTCAGATGCGAACAGA	4711	Db	2694	GAAGCAGGCTACTGAGGAAACTGCTGCTGAGCTGGATAAAGTGGAGGCTTAC	2753
Qy	730	RAISDInHsAlaLysGluGluSerLeuAlaAsp	741	Qy	166	11eCysGlyArgProIleValysProGlu	175
Db	4712	GGAGAGCGTTAGATAAGCAATCTCTTGATGAT	4745	Db	2754	CGGTGCGACTGAGAAAATAAAATGACTTGAACTTGAGAAGTGGTGTGGCCACT	2813
RESULT 7							
US-09-542-615A-119				Qy	176	TyrPheThrGluPheLeuLysAlaValGlnSerLysGlnProProGlnIleGluSer	195
Patent No. 6518256				Db	2814	ATGAGAGCAGAACTACAGAAAGCCAGATCCTGACTTCAAGCTGAGTGTCC	2873
GENERAL INFORMATION:				Qy	196	PhetYProProLeuAspGluProSerIleGlySerIysAsnValAspLeuSerGlyArg	215
APPLICANT: Wang, Tongtong				Db	2874	CTTTAT--GATCTGGACTTGGCAAGTTGGTGAAGAAGTCAACAGCTGACAGCCG	2930
Fan, Linqun				Qy	216	GlnGluArg-----LysGlnIlePhe	222
Kalos, Michael D.				Db	2931	TGGCAAAAGGATAGATAAAAGATCGACTTATGATTATGGGACCTGGGAAACAAATCAG	2990
APPLICANT: Bangur, Chaitanya S.				Qy	223	LysGlyIleSthrPhe-----IlePheLeuAlaAla	232
Hosken, Nancy A.				Db	2991	CAATTGAGGAATTATCGTGTAACTATGAGGCTTTCTGCAAGTGGCTCTATGATCGTAAA	3050
APPLICANT: Fanger, Gary R.				Qy	233	LysGlnHiSlysLysLeuSerSerAlaValPheGlyGlyGlyGluAlaArgLeuLe	252
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY				Db	3051	CGCGCCGAGGATTCCTTAAGATCCATGAAATT-----GGAGATTCCAAACACAGTC	3101
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER				Qy	253	ThrGluGluAsnGluGluLysAsnPhePheLeuAlaProGlyThrCysValAlaAsp	272
CURRENT APPLICATION NUMBER: US/09/542,615A				Db	3102	ATGGGGTTTGTATGGAGCAGAGAATCTG-----	3131
CURRENT FILING DATE: 2000-04-14				Qy	273	ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysSthPheGlnSer	292
NUMBER OF SEQ ID NOS: 350				Db	3132	-----CACAGTCAAATPATCTGCAAACTGAGGAAATCAGAGAAATCAGAAATAAA	3179
SOFTWARE: FastSEQ For Windows Version 3.0				Qy	293	IleValAspMetLeuGlnArgGlnLysLeuArgProGlyLeuGluAlaGluIleLeu	312
SEQ ID NO: 119				Db	3180	ATTCCTGAACTTTCGCCAAATTCA-----ATTAAGGATATGAGCTTCAGCTG	3227
TYPE: DNA				Qy	313	AlaValIlePheMetThrThrLysAsnTyrCysAspProGlyIleHisProSerThrGly	332
ORGANISM: Homo sapien				Db	3228	-----GCC-----TCAAC-----TCAAC-----ACCTCAGGA	3245
US-09-542-615A-119				Qy	333	IeulysThrThrProGlyPro-----SerLeuSerGlnGlyVal	346
Alignment Scores:				Db	3246	CTGAAACTCTGCTGAACTACCTATCAAGAGGACCATGTCCTCTGGG	3305
Pre. No.:	1.44e-06	Length:	8948	Qy	347	SerValAspGlyIleLeuMetProSerAlaProValAspThrThrTyrValAlaAsp	366
Score:	164.50	Matches:	187	Db	3306	ATTCTGCCAAGAGGG-----TGCAAGATGTTCATCTGTAATGGAATCTG	3355
Percent Similarity:	34.23%	Conservative:	132	Qy	367	ThrGluSerGlnAlaAspThrIlePheGlyProIleLeuGlyIleLeuGlyIleLeu	382
Best Local Similarity:	20.06%	Mismatches:	295	Db	3356	-----AGATCTGGAGACTATTACGTTCTTAAGTGAATCTGCTGAA	3397
Query Match:	4.22%	Indels:	319	Qy	382	9GluIleValSerLysMetGluGln-----LysPheArgMetLeuSerGlnAspAlaPr	401
DB:	4	Gaps:	45	Db	3398	GAGTGGAGATCTGAAATAACGAAATGAGATGTTGGAGGAGCTGAG	3457
US-09-837-602-2 (1-754) x US-09-542-615A-119 (1-8948)				Qy	401	OrthrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrIle	421
Qy	2	TrpLysLeuProAlaIleGlyProAlaGlyGlyGluProIleLeuThrGly	21	Db	3458	ACTGCCGAGATGCCAACTCGGAAACACTGTAATAAGAACAAATTCTGATCAAAACCT	3517
Db	2331	TGGATGCTGATG-----		Qy	421	ValAlaCysSerSerCysLeuAsnSerProIleLeuProIleLeuSerProIleLeuSer	441
Qy	22	ValGluItyrValValGlyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSerIle	41	Db	3518	GCAGAAATACGGCAGAGTGTCCAGTCGAGGAGG	3574
Db	2367	AVAGAGACTGGAGGAGGATGACTCTCCTCAAAACCTCCCTAGAACCCGGG---	2423	Qy	441	sSerIysAspArgAla-----	446
Qy	42	SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln	59	Db	3575	GCTGAGAGCAGGGCTGAGTGGAGCTGCTGAGCTGCTGAGCTGCTG	3634
Db	2424	TCTTCCTACCACTACAGTGAATAACGCTTAAGAGCTGTCAGATGATTCAAA	2483	Qy	447	-----SerGlyIle-----SerGlyIle-----	448
Qy	60	ThrAspGluIleLeuThrLeuIleLeuAspSerIleTyrPheValAsn	79	Db			
Db	2484	CCAATTGCTGAGCTTCCTCAACCAAGCTTAAGAT-----ARGCTTGCCAACTTCAGCGT	2537	Qy			
Qy	94	GlyAspGlyIleThrPheGlyIleSerLysPheArgIleGlyIleGluProIle	113	Db			
Db	2538	ATCTATGTTGACTGTTAGTAACTGAGTATTACGAAACTGAAATACTTAACTGACAGTAAG	2597	Qy			
Qy	114	ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeu	133	Db			
Db	2646	-----		Qy			
Qy	134	GlnIleGlyGlyPheThrValAsnAsnIlePheGluCysThrHisLeuValMetVal	153	Db			
Db	2667	CAA-----TTAAAGGTTAT	2693	Qy			
Qy	154	SerValLysValThr-----IleIysThrIleCys-----AlaLeu	165	Db			

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3635 CGGCCAAATAAGAACTCAATGAGAAGATCACCGGACTGACTTATGAGATTGAAAGATGA 3694
 448 nGlnGlnGlnThrAsnSerIleArgAsnTyrPhe----- 459
 3695 AAAGAGAAAGAAATACTGTGGAAAGACAGATTCACAGAAATGACTATGACCA 3754
 459 ----- 459
 3755 ACTGCGAAAGCAAGGCAATGTGAAACCTGGTGGAGAAATTAGAGTCGA 3814
 460 -----
 Qy 460 -----
 Db 3815 GAAAGCCATCAAGGAAAGGGTACCGAGATTGAAAGGTGAGGGTCTACTGCAAGAAGA 3874
 Qy 461 oSerThrLysIleArgGlnLysLeuAspGluGlu-----
 Db 3875 AGGCACCCGGAAAGAGAAATGAGCTGGCAAAGGTAAAGGTTAAGAAACCTATATGA 3934
 Qy 473 nGluMetSerSerCysLysSerIleArgIleGluThrSerCysSerLeuIleGluGlnThr 493
 Db 3935 GGAGATGAGTAATTAAAGAAC---AAAGTAAACAGAAATTACATAGAAAGAACAC 3991
 Qy 493 rGlnProAlaThrProSerIleUrtpIleAsnLysGluGlnHisLeuSerGluAsnGluPr 513
 Db 3992 CATCAAGGAGATA--TCATGCAAAAAGACGATGATTCCAAAATCTAGAAACCAAG-- 4046
 Qy 513 ovalAspThrAsnSerAspAsnSerAsnLeuIlePheThrAspThrAspIleLys---SerIleVa 532
 Db 4047 -CTTGATAGACTTCAAGGAAAT-----CGAGATCTGAAGGATGAATTGT 4093
 Qy 532 LysAsnSerIleSerHisAlaAlaGluLysLeuIleArgSerAsnLysIleSerGln 552
 Db 4094 CAGGCTCAATCACGATCTGCAACGCCATGAGCAGCGAGGCGAGCTGAGAAAACGC 4153
 Qy 552 uMetAspAspPvalAlaIleGluAspGluValLeuPheLysAspThrLysPr 572
 Db 4154 CCTTCAGCAAAAGGCCCTGTGGCTCTGAGATAATGCAAGAAG-----
 Qy 572 oGluLeuGluIleAspValLys---ValGlnLysGlnGluGluAspValAsnValArgly 591
 Db 4199 GCATCTGGAGATAGAACTGAGCAGGTCAATGAGCAGCTCTGGAGCATGCCGGCA 4258
 Qy 591 SargProAspMetAspIleGluIleThrAsnAspThr-----
 Db 4259 CAAGCAGTCCCTGGAG---GAGGCTCAAGACCAATTAGGAGATCGA 4315
 Qy 603 -----
 Db 4316 GAGACTCAAAGCTGACTTCAAGGAGGCC-----AAGGCCGCCCTGGATAATGCA 4366
 Qy 617 uAsnGluIleGlyLysIleAspValLys---AsnGluIleAspValLysGlnLeuIle 635
 Db 4367 AATGAACTGAGTAAGTAAACAATATGAGGAGATCATAGCTTAAATAATCA 4426
 Qy 635 -----
 Db 4427 GTTGAGACCCAGATAAACATCAGGAAACCATCCACAGTCACCATCGAAGGAA 4486
 Qy 636 -GluIleSerAsnAspIleLeuGlnAspSerGluMetLeuProIleLeu-----
 Db 4487 AGAGGTACCCAGTGCTTACCCGGCTCAGATGACAACTCACCCGAGAAAACAGGAGCT 4546
 Qy 655 uLeuIleGluIleArgSerIleValIleLeuIleSerIleSerGlnPr 672
 Db 4547 ATCTGAGAAATAAGGGCTG-----AAGAACACTCTAACCCGACACAGAAACT 4600
 Qy 672 oSerGlyIleAsnAspIlePheGlyLysLeuIleAsnPheIlePheIleSvalrh 692
 Db 4601 CAGGAGGGTGGAAAGACATCCAAG-----GAAAGCCAC 4639
 Qy 692 rTyrProGlyAlaGlyIleLeuProHisIleIleGlySerAspLeuIleAlaHisI 712
 Db 4640 T-----
 Qy 712 SAlaArgLysAsnThrGluLeuGluGluIleLeuIleArgGln-----
 Db 4653 -TCAGAGGAAACAGCAGCTGGGGTGAAGCTCACTCAGATGGCAACAGA 4711
 Qy 730 nABnIinHisAlaLysIleGluIleSerLeuIleAsp 741
 Db 4712 GGAGRCGCTAAGATATAAGCAATCTCTGATGAT 4745
 RESULT 8
 US-09-606-421B-119
 Sequence 119, Application US/09606421B
 Patent No. 6531315
 GENERAL INFORMATION:
 / APPLICANT: Wang, Tongtong
 / APPLICANT: Fan, Ligun
 / APPLICANT: Kails, Michael D.
 / APPLICANT: Bangur, Chaitanya S.
 / APPLICANT: Hobson, Nancy
 / APPLICANT: Panger, Gary R.
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Ajun
 / APPLICANT: Skeiky, Yibir, A.W.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 / TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 / FILE REFERENCE: 210121.455C9
 / CURRENT APPLICATION NUMBER: US/09/606,421B
 / CURRENT FILING DATE: 2000-06-28
 / NUMBER OF SEQ ID NOS: 358
 / SOFTWARE: FastSSQ for Windows Version 3.0
 / SEQ ID NO: 119
 / LENGTH: 8948
 / TYPE: DNA
 / ORGANISM: Homo sapien
 US-09-606-421B-119
 Alignment Score:
 Pred. No.: 1.44e-06
 Score: 164.50
 Percent Similarity: 34.23%
 Best Local Similarity: 20.06%
 Query Match: 4.22%
 DB: 4
 DB: 45
 US-09-837-602-2 (1-754) x US-09-606-421B-119 (1-8948)
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 Db 2331 TGGAGCTGATG-----
 Qy 22 ValGluIleValValGlyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSerIle 41
 Db 2367 ATAGGCACTGCGAGGCGAGATGACTCTCAAAACCTCCCTGAGCACCGGG--- 2423
 Qy 42 SerArgAsnHisAlaValIleThrIleAlaAsn-----
 Db 2424 TCTTGTACCATACAGTAAAGAGCTAAAGTGTCAAGATGATTCAAA 2433
 Qy 60 ThrpGluIleProValLeuIleLeuIleAspAspSerIleIleGlyThrPheValAsn 79
 Db 2484 GCAATGCTGAGGTCTCAACCGGTTAAAGAT-----ATGCTTGCCAAACTTCGAGGT 2537
 Qy 80 GluGluIleS-----MetGlnAsn-----
 Db 2538 TCTGAAAGTACTGGTATTACAGATGAGTATTGACTATTTCAGAAACTGGAAAT 2597
 Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerIleSpheArgIleGluIleGluProLeu 113
 Db 2598 ATCATGGCTTACGATGCTACTTAATAGCTATGCAAGTATGCAAGTCAAA 2645
 Qy 114 ValAlaCysSerSerCysIleLeuAspValSerGlyIleSthAlaLeuAsnGlnAlaIleLeu 133
 Db 2666 -----
 GCACCTGCTCAGGGCTTCTTC

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QY	134 GlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGlyCysThrHisLeuValMetVal	153	441 bSerLysAspArgGala-----	446
Db	2667 CAA-----ACAGAGAGATG-----TAAGGTTAT	2693	Db : : : : : :	
QY	154 ServallysValThr---IleLysThrIleCys-----AlaLeu	165	QY 447 -----	SerG1 448
Db	2694 GAAGCCGGCTACTGAGGAARCTGTCGCTGGAACTGGAGCTAC	2753	Db 3635 CGCCCAATAAAGAACTCAATGAGAAGATACCCGACTGACTTATGAGATGAAAGATGA	3694
QY	166 IleCysGlyArgProlleValLysProGlu-----	175	QY 448 nGlnGlnGlnThrSerSerIleArgAsnThrPhe-----	
Db	2754 CGCTGTTGACTGAAGAAATAATGACTTGAACTTGAAAGACTGCTGTCGACTGCCACT	2813	Db 3695 AAAGAGAAAGAAATACTGTGAAAGACAGATTGACCAAACTGAGATGACTATGACCA	3754
QY	176 TyrPheThrGluPheLeuLysAlaValGlnSerIleLysGlnProGlnIleGluSer	195	QY 459 -----	
Db	2814 ATGAAAGAGAACTACAGAACTGCAACTCTCAGACTTCAGCAGTATCCA	2873	Db 3755 ACTCGAGAAAGGCAATGTCGAAAGGAGACCTTGGTGGCAGAAATTAGAGTCYGA	3814
QY	196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArg	215	QY 460 -----	GlnPr 461
Db	2874 CTTAT---GATCTGGACTTGGCAAAGTCACTGAAACAACTCACAGCTGACGACCC	2930	Db 3815 GAAAGCCATCAAGGAAAGGGATGACAGAGATTGAAAGGTGAGGGTCTACTGAGGAGA	3874
QY	216 GlnGluArg-----	222	QY 461 oSerThrLysArgGluIaArgAspGluGlu-----	ABnG1 473
Db	2931 TGGCAAAGGATAGATAAACAGATGACTTGGATTATGGACCTCGTGTGAAACAAATCAG	2990	Db 3875 AGGACCCGAAAGGAGATATGAAATGAGCTGGCAAGGTAAGGTAAGGTCAGCTGAA	
QY	223 LysGlyLysThrPhe-----	232	QY 473 nGluMetSerSerCysLysSerAlaArgIleGluThrSerLeuLeuGluGlnThr	493
Db	2991 CAATTCAGGAAATTATGCTGATAACTATCAGCTTCTGCAAGTGGCTCATGCTGAA	3050	Db 3935 GGAGATGACTAAATTAAAGAACAC-----AAAGTAAAGAACATTAAGAGAACCC	3991
QY	233 LysGlnHisLysLysLeuSerAlaValValPheGlyGlyGluAlaArgLeuIle	252	QY 493 rGlnProAlaThrProSerLeuLeuTrpLysAsnGlnHisLeuSerGluAsnGluPr	513
Db	3051 CGCCGCAGGATTCCCTTAAGTCAACACAGTC	3101	Db 3992 CATCAAGGAGATA---TCATGCAAAAGGAGGTGATTCCTAACATGAAACACAGC	4046
QY	253 ThrGluGlyIleThrLeuAsnPheLeuAlaProGlyThrCysValValApp	272	QY 513 ovalAspThrAsnSerAspAsnAsnLeuPheThrAspPheLysAspLeuLys---SerIleVa	532
Db	3102 ATGGCGTTTGTGAATAGCAGAAGAACTG-----	3131	Db 4047 -CTGATAGACTTCAAGGAAATT-----CGAGATCTGAGGTGAATGTAATGT	4093
QY	273 ThrGlyIleThrLeuSerGlnThrLeuIleProAspCysGlnLysThrPheGlnSer	292	Db 532 lLysAsnSerAlaSerLysSerAlaGluIleGluAspGluValLeuGluGlnLeuPheLysAspThrLysPr	552
Db	3132 -----CACAGTGAATAATCTGGCAAAACGAGACAATCAGGAGATCAAAA	3179	Db 4094 CAGCTCAATGAGCACTATCTGCAAGGCCACTGAGCAATGAGCTGAAGAAACCC	4153
QY	293 IleMetAspMetLeuGlnArgGlnIleLeuArgProIleGluAlaGluIleLeu	3112	QY 552 uMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLysPr	572
Db	3180 ATTGCTGAACTTTGCCTAACATICA-----ATTAGGATTATGAGCTCAGCTG	3227	Db 4154 CCTTAGGCAAAAGGCCCTGAGCTCTGAGATAATTCGAGAG-----AAAGCA	4198
QY	313 AlavaIlePheMetThrThrLysAsnThrCysAspProGlnGlyHiSProSerThrGly	332	QY 572 oGluLeuGluIleAspValLys---ValGlnLysGlnGluGluAspValAsnValArgLys	591
Db	3228 GCTAC-----TCATAC-----ACCTCAGGA	3245	Db 4199 GCATCTGGAGATAGAAGCTGAGCTGAGCAATGCCGGCA-----AACTG	4258
QY	333 LeuLysThrThrThrProGlyPro-----SerLeuSerGlnGlyVal	346	QY 591 sArgProArgMetAspIleGluIleAspValLys-----	602
Db	3246 CTGGAAACTCTGCTGAACTATCAAGGGACCATCTTCAAGCTCCCTCTGGGTRG	3305	Db 4259 CAAGGAGTCGCCAGACCCATTCTGGACAAATAAGGGATCATGATCGA	4315
QY	347 7 servAlAspGluIleMetProAspAlaproValAsnThrThrTyraValAlaAbp	366	QY 603 -----PheSerAspGluAlaValProGluUserSerLysIleSerGlnG1	617
Db	3306 ATTCTGCAAGAGGC-TGCAAGATGTTCTGCTGGTACATGCAACTACTAC	3355	Db 4316 GAGACTCAAAGCTGAGTTCTGAGGAGGCC-----AAGCCCGCTGGAAATATGA	4366
QY	367 ThrGluSerGlnGluIleAspThrTrpAsp-----LeuSerGluArgProLys	382	QY 617 uAsnGluIleGlyLysBlaArgGluLeuLysGluAspSerLeuTrpSerAlaLys	635
Db	3356 -----AAGATCTGCAAGACTATTACGGTTCTTAAGGAGATGCTGAA	3397	Db 4367 AAATGAACTGAGTAAAGGAGATCATGAGGAGATCATGATGAAACAAATTTAAATCA	4426
QY	382 8GluLysValSerLysMetGluGln-----LysPheArgMetLeuSerGlnAspAlaPr	401	QY 635 -----AAATGAACTGAGTAAAGGAGATCATGAGGAGATCATGATGAAACAAATTTAAATCA	635
Db	3398 GAGTTGAGACCGAGATCAACATCACAAAGCACCCTTCACAGCTCACCATGAGCAAGGA	3457	Db 4427 GTTGAGACCGAGATCAACATCACAAAGCACCCTTCACAGCTCACCATGAGCAAGGA	4486
QY	401 othrvalLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLe	421	Db 636 -GluLysSerAsnAsnAspSerGluMetLeuProLysLeuLe	655
Db	3458 ACTGGCCGAGATGCCAACTCGGAAACTGTTATAAGAACAAATTCGGATCAGAACCT	3517	Db 4487 AGAGGATAACCTGCTGCTACGGCTCAGATAGACATCTCACCCGAGAAAACGAGAGCT	4546
QY	421 uAlaLysMetArgIleProAsnProThrSerProIleLeuSerIleAsnLys	441	QY 655 uLeuThrGluPheArgSerLeuValLeuLysAsnSer-----ThrSerArgAsnPr	672
Db	3518 GCAGAAATAACCGCAGACTGTCGTCAGCTGAGCTGAGCTGAGCA	3574	Db 4547 ATCTGAGAAATAAGGAGCTG-----AAGAACCTCTAACCCGACGACGAACTCT	4600
QY	672 oSerGlyIleAsnAspAspPheLysThrGlyGlnLeuLysAsnPhenLysLys		QY 672 oSerGlyIleAsnAspAspPheLysThrGlyGlnLeuLysAsnPhenLysLys	692

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Qy	429 rGlnleuSerProThrLys-----Le	436	717 rGlubeuGluGluTrpLeuArgGlnGluMetGluValGlnHisAlaLysGluG1	737
Db	1305 TCCCTCA GTGAA CAGGAA TAAAGCTAAACGAAATTAAAGGCTAAAGAACGAGTACTGGCT	1364	Db 2259 TGATCTTCAGAAAGACTAAATAAAAGATGAA --GAATAGAGCTTGGGAAAGA	2315
Qy	436 uProSerLleAsnLysSerLysAspDArgAlaSerGlnGlnThrAsnSerLleA	456	Qy 737 u	737
Db	1365 TGGCAAAATTAACTAAATGAGAAC--TCAAACTATGGATTAATATACCAAC	1421	Db 2316 A 2316	
Qy	456 gAsntryPheGlnProSerThrLys-----LysArgGluGargAspGluG1	471	RESULT 10	
Db	1422 ADATAACACAAACATAAGCTTCTATACTGAAATTGTGAATC	1481	US-09-220-132-79	
Qy	471 uAsnGlnGluMetSerSerCysLysSerAlaArgLleGluThrSerCysSerleLeuG1	491	Sequence 79, Application US/09220132	
Db	1482 TGTCTGTTAGAGCTGATGTTCACTGAACTTAATGTGAGATA	1536	Patent No. 6506607	
Qy	491 uGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluG1	511	GENERAL INFORMATION:	
Db	1537 -GAATGGAATCCAGCAACAAAGCTACTA-----AATCAGGAAATATAAGAAACTGAGTT	1589	APPLICANT: Shyian, Andrew W.	
Qy	511 nGluProValAlaPheThrAsnSerAspAsnAlnLeuPheThrAspThrAspLeuLysSerI1	531	METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT	
Db	1590 GAACTCACACTGCTGCTGATGATGATACTGGTTAGACTATGAACTACAAACA	1647	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT	
Qy	531 eVallysAsnSerLysSerSerHisAlaAlaLysLysSerAsnLysLysBar	551	OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER	
Db	1648 -----GAAGAAAGAGAAATGGAAATTGAAATTAAA-----GAAAGAA	1685	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT	
Qy	551 gGluMetAspAspPvalAlaLleGluAspGluValLleGluLysAspThrI1	571	FILE REFERENCE: 07334-074001	
Db	1686 TGATTGGAT-----GATTGGGGCTAGATGAAAGAAACTAAAGATCA	1733	CURRENT APPLICATION NUMBER: US/09/220, 132	
Qy	571 sProGluLeuGluLleAspValLysValGlnLysCinGluAspValAsnValArgLys	591	CURRENT FILING DATE: 1998-12-03	
Db	1734 A---GAGATCCTAACCTAACCTGAAATTCTGAAATTAGTTAACGCTTCGAGA	1790	PRIOR APPLICATION NUMBER: US 60/079, 303	
Qy	591 sArgProArgMetAspIleGluLysAsnAspThrPheSerAspGluAlaValProGluSe	611	PRIOR FILING DATE: 1998-03-25	
Db	1791 AGTATAATACTAACATCT-----	1809	PRIOR APPLICATION NUMBER: US 60/068, 821	
Qy	611 rSerLysIleSerGlnGluAsnGluIleGlyLysLysArgGluIeu-----LysG1	628	NUMBER OF SEQ ID NOS.: 191	
Db	1810 -----GAGATGAACTCACTGAACTTCTGAACTTCTGCTAGAGAAAGGA	1853	SOFTWARE: FastSBQ for Windows Version 4.0	
Qy	628 uAspSerLeuTrpSerAlaLysGluIleSerAsnAsnAspLysLeuGlnAsp-----	645	SEQ ID NO.: 79	
Db	1854 AGCCAGATAAGGACTACAGATACTAGATACTCTCTCCTAAAGCTGAAATAATATAAAAT	1913	TYPE: DNA	
Qy	646 -----AspSerGluMetLeuProLysLeuLeuIleGluLys	659	ORGANISM: Homo sapiens	
Db	1914 GGACTTGTCTACTCATGGAAAGGATTGAGAACCCAAACAAATGAAAGCAGACTCTGTT	1973	US-09-220-132-79	
Qy	659 eArgSerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAsp	678	Alignment Scores:	
Db	1974 TGAATCTGAAACTGTAGCCCAAGAGAAATCAGCTTCTAGAAAGTGAAGAAA	2033	Length: 1.16e-06	
Qy	679 -----TyrGlyGlnLeuLysAsn-----	684	Score: 162.50	
Db	2034 TCTGGAGTGTGAAAGGAGAAAATGAAGAAACTTGTGATACTACATAAGGAAATATG	2093	Percent Similarity: 37.50%	
Qy	684 -----AspSerGluMetLeuProLysLeuLeuIleGluLys	684	Best Local Similarity: 20.70%	
Db	2094 TATTCAGTTATCAAAGGCAATTGGAGGAAAAAATGCAAGTGTGATCTGGAGAA	2153	Query Match: 4.17%	
Qy	685 -----PhenylSlysPhenylSlysValThrTyrProGlyAlaGlyLysLe	699	DB: 4	
Db	2154 AGAATTACAACTCTGTTTAATGAGATAAAACTACACTCCCTATAGTGGAAAGT	2213	Length: 1.16e-06	
Qy	699 uProHisIleIleGlyGlySerAspLeuIleAlaHis-----HisAlaArgLysAsnTh	717	Score: 162.50	
Db	2214 TCCAA-----AAAGATTGCTGCTGATTGCAATTGGAAAGCAAAATTAC	2258	Percent Similarity: 37.50%	
Qy	700 -----LeuAlaLysMetArgIleProAsnTyrgIleLeuSerProThrLysLeuProSerIleAsn	740	Best Local Similarity: 20.70%	
Db	2259 TGATCTTCAGAAAGACTAAATAAGGAAACTGAGCTTGGGAAAGA	2313	Query Match: 4.17%	
Qy	740 -----LeuAlaLysMetArgIleProAsnTyrgIleLeuSerProThrLysLeuProSerIleAsn	740	DB: 4	
Db	2316 A 2316		Length: 1.16e-06	
Qy	741 LysSerLysAspArgAlaSerGlnGlnGln-----ThrAsnSerIle	745	Score: 162.50	
Db	2317 AACGATTAATGCTGAAAGAAAGATGAGATGTAGAGAAATACAGCT	2997	Percent Similarity: 37.50%	
Qy	744 AACGATTAATGCTGAAAGAAAGATGAGATGTAGAGAAATACAGCT	2998	Best Local Similarity: 20.70%	
Db	2998 AACGATTAATGCTGAAAGAAAGATGAGATGTAGAGAAATACAGCT	3057	Query Match: 4.17%	

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Qy 456 ArgAsnTyrPheGinProSerThrLysArgGluuArgAspGluuAsnGlnGluMet 475
 Db 3058 GAACGAGCCAGCAGCTGAAAGCAGCTAAAGCATGGAAAGAAAGATTGGAGGG 3117

Qy 476 Ser---SerCysLysSerAlaArgIleGluThrSer-----CysSerLeuLeuGlu 491
 Db 3118 AAATGTCGACCTCTGGAAAGAAATGGAAACAAACACTGTCAAGGCTGAA 3177

Qy 492 GluThrGlnProAlaThrProSerLeuIlePheAsnLysGluGlnHisSerSerGluAla 511
 Db 3178 GCCAGCTATGAGAGGCCATTCTGAGAAAACAGGATGAGAAATCCTACAGAC 3237

Qy 512 GluProValAspThrAsnSerAspAsnAsnLeuPheAspThrAspIleAspIle 531
 Db 3238 -----CTCCAGAAAGCCTGCTGGACACAGGAAAGCTGAAGGGCA 3282

Qy 532 VallysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAlnLysArg 551
 Db 3283 CGGGAGGAGAACAGTGGCTGCTGCAGGAGCTGGAGGAAGCCGACAAA 3342

Qy 552 GluMetAspAspPvalAlaIleGluAsp-----GluValLeuGluGlnLeuPheAsp 568
 Db 3343 GCCAAAGCTGTCTCAAACAGGGGAAATGCCATGCGAGATAATGGAACAGTGAACAGGAG 3402

Qy 569 -----AspThrLysProGluLeuGluIleAspValIle 579
 Db 3403 AGAGCTGAGACTCTGGCTCCTGGAGAACTGGCAAG-----CAACAAAAATGCAAA 3453

Qy 580 ValGln-----LysGlnGluGluAspValAla 588
 Db 3454 CTACAGAAATGAAATTGGACACACTTAAAGAAAACAACTTGGAAAGCTGAAAC 3513

Qy 589 ValAspGlySerGlyPro-----ArgMetAspIle 597
 Db 3514 AAATCAAAGAAACTCTGACTGTAGAGATCATAAAATGGAAAGAAATTAGGAAGAAATA 3573

Qy 598 GluThrAspThrPheSerAspGluuIleValProGluSerLysLeuSerGlnGlu 617
 Db 3574 GAAACCCTAACGCCAGGCCGCTCAGAGTCCCGCAAGTTCAAGGTGCAAGAAGG 3633

Qy 618 Asn-----GluIleGlyLysArgGluuIleIuylsGluuAspSerLeuTerP 632
 Db 3634 AACGTTAAACTTGCTGAGGACCTGGGAAGACGGAC 3672

Qy 633 SerAlaLysGluIleSerAlaAsnAspLysLeuGlnAspSerGluMetLeuProIle 652
 Db 3673 -----GAAAGTCACAAGTCATCAAACGCTGGAGAAAGATCTGGCTCAAATAAT 3723

Qy 653 LysLeuLeuIleThrGluuIleArgSerLeuValIleLysAsnSerThrSerArgAsnPro 672
 Db 3724 CAGTTAA-----GAAATGAAAGAAATCC 3753

Qy 673 SerGlyIleAsnAspPheSerPheGlyGlnLeuLysAsnPhenylsLysSerValThr 692
 Db 3754 AAGTTCATAAAAGACCCAGATGAAGAAAGCTTCCTGGAAATCCATCAGPATAACT 3813

Qy 693 TyrProGlyAlaGlyLysLeuProIleIleGlySerAspLeuIleAlaIshIsh 712
 Db 3814 -----AGTGCCTTACTC----- 3825

Qy 713 AlaArgLysSerThrGluuIleGluuIleLeuIuylsGluuIleIuylsSerValThr 731
 Db 3826 ACAGAAAAGGATGCCAGCTGGAGAAA-----CTGAGAAATAGGTCAAGCTCAAGGGAA 3882

Qy 732 GlnHisAlaIysGluuSerLeu 739
 Db 3883 GAAAACGCTCTGGCAAGTCCTTG 3906

Qy RESULT 11
 Db Sequence 1575 Application US/09107532A
 Db Patent No. 6583275
 Db GENERAL INFORMATION:

Qy 97 ethrPheGlyValPheGlySerIlePheArgIleGluuIleGluuProLeuValAlaCysSe 117
 Db 348 AACGTTGACCATTTGATGGAAAGGGAAA-----

APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: JULY 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinelli, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 893-5007
 TELEFAX: (781) 893-8277
 INFORMATION FOR SEQ ID NO: 1575:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...3135
 SEQUENCE DESCRIPTION: SEQ ID NO: 1575:
 US-09-107-532A-1575

Alignment Scores:
 Pred. No.: 4.57e-07
 Score: 162.00
 Percent Similarity: 32.92%
 Best Local Similarity: 17.97%
 Query Match: 4.15%
 DB: 4
 DB: 4
 US-09-837-602-2 (1-754) x US-09-107-532A-1575 (1-3135)

Qy 51 AsnProSerValThrAsnLeuSerGlnThrAspGluuIleProValLeuThrLeuLysAsp 70
 Db 168 AACCTCCGGAAAGACTTCGCTCTGGAAAGAGATCGGTTCTTGCTACACCGACGA 227
 Qy 71 AsnSerLysTyrGlyThrHeval----- 71
 Db 228 AGAAACAAAGCTGACATTCTCTTCTTGAACATCAGAGATGAGCTATGAAATCGAACGAA 287
 Qy 83 MetGlnAsnGlyPheSerArgThr-----LeuLysSerGlyAsp-GlyIle 97
 Db 288 ACCAACACAGTTAGCAAACAAAAGGAAACAAAACAGCAGCAAAG 347
 Qy 97 ethrPheGlyValPheGlySerIlePheArgIleGluuIleGluuProLeuValAlaCysSe 117
 Db 348 AACGTTGACCATTTGATGGAAAGGGAAA-----

DE3 | AVAILABLE

MOLECULE TYPE: cDNA
 FEATURE: CDS
 NAME/KEY: 1 .. 3294
 LOCATION: US -08-923-992A-7

Alignment Scores:
 Pred. No.: 6..39e-07 Length: 3294
 Score: 161..00 Matches: 141
 Percent Similarity: 37.11% Conservative: 124
 Best Local Similarity: 19.75% Mismatches: 233
 Query Match: 4..13% Indels: 216
 DB: 3 Gaps: 39

US-09-837-602-2 (1-754) x US-08-923-992A-7 (1-3294)

Qy 192 GluIleSerPheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp 211
 Qy 298 CAGAAAATAGCTTAAACAAAATCTGATAAACATGATTCTGATCATGATTAGAA 357
 Db 212 LeuSerGlyArg ---
 Db 358 TAGAAAATCAATTAAACGAAACTATAGCTTACATCAACAAACATGAGAAAGTT 417
 Qy 222 PheLysGlyLysThrPheLeuAsnAlaLysGlnHisLysLysLeuSerSerAla 241
 Qy 418 GAGAAAGATAAG---
 Db 242 ValAlPheGlyGlyGluAlaArgLeuIleThrGluGluGluGluHisAsn 261
 Db 463 -----
 Qy 262 PhePheLeuAlaProGlyThrCysValAlaLeuAspThrGlyIleIleAsnSerGlnThrLeu 281
 Db 505 CATCAAAAAGTCAA-----
 Qy 282 IleProAspCysGlnLysLysTTPileGlnSerIleMetAspMettLenglnArgGlnGly 301
 Db 544 --AAAGATTCTATGCTGAAAAAATTCGAAGATATTCTAAACAGCTAACACAGAT 600
 Qy 302 LeuArgProlleProGluAlaGluIle-----GlyLeuAlaValIlePheMetThrThr 319
 Db 601 AAAAAGAGAGATGCCGAGTAAGGTCTGTAAGAACTTGTAAACCTCTGTTCAACT 660
 Qy 320 LysAsnIleThrCysAspPto-----GlnGlyHisProSerThrGlyLeuIleThrThr 337
 Db 661 AAAGCTGGTCGGATCAAGAAATTCAAGAGGCAT-----GTGAGAAAGAAACG 708
 Qy 338 ProGlyProSerIleSerGlnGlyValSerIleAspGluLysLeuMetProSerAlaPro 357
 Db 709 ACTAGTGGAGAAATACTCAG-----AAAGTGTATGAGACACTAT-----747
 Qy 358 ValAsnThrThrThrTyrvAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeu 377
 Db 748 GCTATAAGCCCTCAGAACCTTCGCTCAAAATCTCTGAGAAACTGATAAGGCAACTTAC 807
 Qy 378 SerGluIleArgProLysGluIleSerLysMetGlu-----GlnLys-----392
 Db 808 AATGAAACAGCTAACAGTAAACATCTTAAAGCTAACATCTTAAAGCTAACAGAA 867
 Qy 393 -----
 Db 401 ProThrValLysGluUserCysLysIleSerSerAsnAsn-----SerMvaValSer 418
 Db 928 GAGCAGCTTGAGAGGAAATTAAACATAATTCTGAGATTCTGTTGGCG 987
 Qy 419 AsnThrLeuAlaLysMetArgIleProAsnIleProThrLys-----LeuPro 437
 Db 868 ATACAACCTCTATCAAGAAACGAAATGTGAAATTGATAAGGCTATGAGACGTRG 927
 Qy

RESULT 12

US-08-923-992A-7

Sequence 7, Application US/089221992A
 Patent No. 6280738

GENERAL INFORMATION:

APPLICANT: Tai, Joseph Y.
 APPLICANT: Blake, Milan S.
 TITLE OF INVENTION: No. 6280738-19A Fc Binding Forms of the Group B
 TITLE OF INVENTION: Streptococcal Beta Antigens
 NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,992A
 FILING DATE: 05-SEP-1997
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/024,707
 FILING DATE: 06-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1438.0140001/RWE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3294 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

438 SerIleAsnLysSerLysSerLysSerAspAspAla 400

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NUMBER OF SEQ ID NOS:	5
SOFTWARE:	FastSEQ for Windows Version 3.0
SEQ ID NO 1	
LENGTH:	2815
TYPE: DNA	
ORGANISM:	Homo sapiens
FEATURE:	
NAME/KEY: CDS	
LOCATION: 110..2371	
NAME/KEY: unsure	
LOCATION: 46..46	
OTHER INFORMATION: n = a, c, g or t	
NAME/KEY: unsure	
LOCATION: 2731..2731	
NAME/KEY: unsure	
LOCATION: 4..4	
OTHER INFORMATION: n = a, c, g or t	
US-09-214-5644A-1	
Alingment Scores:	
Pred. No.:	1.18e-06
Score:	157.50
Percent Similarity:	31.92%
Best Local Similarity:	18.90%
Query Match:	4.04%
DB:	3
US-09-837-602-2 (1-754) x US-09-214-564A-1 (1-2815)	
Qy	59 GlnThrAspGluIleProValLeuThrLeuIysAspAsnSerLysTyrGlyThr-----
Qy	599 CAGAGGAGGAACTTACAGATTAAGGTAATCTAA-----GGAATCTTAA 652
Db	777 -----PheValAsnGluGlyIleMetGlnAsnGlyPheSerArgThr 90
Qy	653 GGAGACGGCTCTTGTGTTATTGAAAGGAACTCTGGAA-----CITGCA 700
Qy	91 LeuIysSerGlyAsp-----GlyIleThrPheGlyValPheGlySerIys 105
Db	701 TAAAAACTTTGGATGAAGATGAAATTAGGGCTACAAATTACATGTTGAGGTGGCAAG 760
Qy	106 PheArgIle-----GlutyrGluProLeuValAlaCysSerSerCysLeuAspValser 123
Db	761 TTCACTGAGGGAAATAATGCTCAAGAAGAGAAGAAGCTATAAG 820
Qy	124 GlyLysThrAlaLeuAsnGlnAlaLeuIysLeuGlyIleGlyPheThrValAsnAsnTyr 143
Db	821 AGAACCTGCTATGCCAACAAAGCAACTG-----GATTGG 856
Qy	144 ThrGluGlu-----CysteThrHis-----
Qy	857 AGACCTGAGGGAGCGGACCATCGGGATGAGCTGTCATCAAG 916
Db	150 -----LeuValMetValSerValVal 157
Qy	917 ATAATGTTCTCCATGGATTGAGGATCTGGCTGAATGAGATCAGAGA 976
Db	158 ThrIleIysThrIleCysAlaLeuIleCysGlyArgProIleValysProdItyPhe 177
Qy	977 GACCTTCGAGAGTCCTG-----
Db	178 ThrGluIleLeuAlaValAlaIysSerIysLeuIysLeuIysSerIysLeuAsn 195
Qy	1004 CGACAAATTAGGAAACTCTCTCTGATGGCACCGAGATGGCTCTGNGTCC 1063
Db	196 Phetyr-ProProLeuAspGluProSerIleGlySerIysAsnValAsp-----Leu 212
Qy	1064 TTTCGGGATCA---GAGGAACCTGATACTGTTATGATTCGATGAGATGGTT 1120
Db	213 SerGlyArgGInGluArgLysClnIlePhenylsGlyLysThrPhenylsPheLeuAsnAla 232
Db	1121 GCGGCCGTCAAATCACTGCCAACGGATGGCATGGACTCA-----
Qy	233 IysGlnIhsIlysLeuSerSerAlaValAlaPheGlyGlyGluAlaArgLeuIle 252
Db	1163 -----GATPATCAGTTGGAGGAACCC 1183
Qy	253 ThrGluIleAsnGluGluGluHiAsnPheLeuAlaProGlyThrCysValAsp 272
Db	1184 TCAAGAAAGGGAGGAAGG-----
Qy	273 ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSer 292
Db	1205 -----CTGAGAGGATG-----
Qy	293 IleMetAspMetLeuGlnArgGInGlyLeuArgProIleProGluAlaGlyIleLeu 312
Db	1217 -----GAGGCTTCCTCAATGCTCCTGAGCCACAGGCTT 1255
Qy	313 AlaValIlePheMetThrThrAsnIysCysAspPro-----Gln 326
Db	1256 AGGGTTCAGATTCTGTCCTGCTGCTGAGCAAGGCAAGGGCTCTAGAGCAAGGCTATTCTCA 1315
Qy	327 GlyHisProSerThrGly-----
Db	1316 GRCGACCCCAAGCACATCTAAAATGAATGCTCAAGAAACTGCAACTGGAATGGCATTGTAA 1375
Qy	333 -----LeuIysThrThrProSerIleSerGlnGly 345
Db	1317 GAACTATAGATGAGAAAGGTTGAAGAAGGAAATTGAGAGGT 1435
Qy	344 ValSerValAspGluIlysLeuMetProSerAlaProValAsnThrThrThrThrValAla 365
Db	1436 GCTTCGAAACAACTGCTAAGGAAAGTACCCCGAAAAGAGGCTGAGAGGCTGCCCT 1495
Qy	366 AspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluIysGluIys 385
Db	1496 GAAAGAGATCTGAAAGGGC-----TGCCCCAAAAGGGCTTGAAGGCAGC 1543
Qy	386 ValSerIlysMetGluGlnIys-----PheArgMetLeuSerGinAspAlaPro 401
Db	1544 TGCTTCGAAAGGCTGAGAGGCTACCCGTAAGGCAATCCCGTAAGGCTGAGAGGATGTC 1603
Qy	402 ThrValIysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeu 421
Db	1604 -----AAAAAAAGCTTAAAGAGAACACTCAAAAATGATTGAGAAGAAATGCTGCCRT 1657
Qy	422 AlaIys-----MetArgIleProAsnItyGlnLeuSerProThrIlys 435
Db	1658 GCAGAGGAATCTGAAGATGACCTCAACAGGAGTCGCTGAGGAGGTTGACGGCTTGCCCAQAAA 1717
Qy	436 Leu-----ProSerIleAsnIysSerIlysAspArgAlaSerGinGlnGln 451
Db	1718 GAGTCGAGGAAGGAGACTCTGAGAAAGACTCTGAGAAAGACTGCTGAGAAAAGCTGCT 1777
Qy	452 ThrAsnSerIleArgAsnItyPheGlnProSerThrIlysIysSerIlysAspIleLeuIysSerIlys 471
Db	1778 GAGATGGCTCCGAGAAAGGAAATTTGAGAAAAGATTGACGGCTTGACGGAA 1837
Qy	472 AsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuIleGlu 491
Db	1838 GGTTCGAA-----
Qy	492 GlnThrGlnProAlaThrProSerIleTrpIysAsnIysLeuIysSerGluAsn 511
Db	1847 -----AGGAGCTTCATGAAATAATGTTCTGCAAAAAGCTGCT 1876
Qy	512 GluProValAspThrAsnSerAspAsnAspIlePheThrAspThrAspIleIysSerIleIys 531
Db	1877 GAGTAGAGAAAGATTGACTCTGAAAATCTCGAAATTTGAGATGAGGGCTCTGAAAGAGTG 1936
Qy	532 VallySerAlaSerIleSerIlysSerIlysLeuIysArgSerAsnIlysIlysBarg 551
Db	1937 TTAGATGAGAAAGCTCTGAGGAGTTGACGAAT-----TCAGATGAAAGGGAA 1990
Qy	552 GluMetAspDaspValAlaIleGluAspGluValleIleGluIlePhenylsAspThrIlys 571
Db	1991 GAA-----GAGGGAGACATATGAAAGTTTGTATGAGTGTCT 2032

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Percent Similarity: 36.96%
 Best Local Similarity: 20.05%
 Query Match: 4.03%
 DB: 1 Gaps: 40

US-09-837-602-2 (1-754) x US-08-242-932-1 (1-4200)

Qy 572 ProGluLeuGluIleAspValLysValGlnLysGlnGluGluAspValAsnValArgLys 591
 Db 2033 GATGAAAGAG-----GATGAAAGATATGCAGATGAAAGGGG 2071

Qy 592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal---ProGlu 610
 Db 2072 CTTGAACTGCTGATAAAAGCGGAAGAACGGTGTGAGTGTGAAAGAG 2131

Qy 611 SerSerLysIleSerGlnGluAsnGluIleLysLysArgGluLeuLysGluAspSer 630
 Db 2132 TCGATGCAAGGAAAGATGAGATGAGATGAGATGAGATGACCAAAAG 2191

Qy 631 LeuTrpSerAlaLysGluIleSerAsnAspLysLeuGlnAspAspSerGluMetLeu 650
 Db 2192 TTGTRTC-----GAAGATGATGATTCATGAGAAGTTGTTGATGAGCGGAGATTC 2245

Qy 651 ProLysYleLeuLeuThrGluPheAspSerLeuValIleAsnSerThrSerArg 670
 Db 2246 AGTGAAGATGTTT----- 2260

Qy 671 AsnProSerGlyIleAsnAspAspTyrGlyGlnLeuLysAsnPheLysLys-PheLysLys 690
 Db 2261 -----GACGATCTCTGATGAGACGGGGACCTTGGGGCTTGGGACTGTTGAAGGA 2311

Qy 690 SVALThrTyrProGlyAlaGlyLysIle 699
 Db 2312 GGGCCCTATCCACTGGCACAGCTTA 2339

RESULT 15
 US-08-242-932-1
 sequence 1, Application US/08242932
 Patent No. 5595740

GENERAL INFORMATION:
 APPLICANT: Brady, L. Jeannine
 TITLE OF INVENTION: Cloning of No. 5595740-1GA Fc Binding Forms of
 NUMBER OF SEQUENCES: 8
 TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik, E. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/242, 932
 FILING DATE: 16-MAY-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: UF142
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4200 base pairs
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-242-932-1
 Alignment Scores:
 Align. No.: 2.63e-06
 Score: 157.00
 Length: 4200
 Matches: 144
 Gaps: 483

Percent Similarity: 121
 Best Local Similarity: 236
 Query Match: 4.03%
 DB: 1 Gaps: 40

Qy 192 GlnIleGluSerPheThrPheProProSerGluLysGlySerLysAsnValAsp 211
 Db 710 CAGAAAATAGTTAAACAAATTTGATGAAACAAATGATTCTGATTGATTAGAA 769

Qy 212 LeuSerGlyArg-----GlnGluArgLysAsnIle 221
 Db 770 TTGAAATACTTAACTGAAACTATGACTGTTACACATCAACAAACATGAAAGTT 829

Qy 222 PheLysGlyLysThrPheIlePheLeuAsnAlaLysGlnHisLysLeuSerSerAla 241
 Db 830 GAGAGATAG-----AAAGCTAGGCAACAGAACAGAACACTGAAACAGCTCA 874

Qy 242 -----ValValPheGlyGlyLysLysGluIalArgLeuIleThiGluIuaAsnGlu 258
 Db 875 GATAGAAAGTAGATGATCTAACCAATTGCAAAAGGCTTAATCATCAAANAAAGTCAAGTT 934

Qy 259 GluHisAsnPheLeuIleAlaProGlyIleThrCysValValAspThrGlyIleThrAsnSer 278
 Db 935 GAA-----AAAGATCTCTATGCTGAAAAAATGCAAAAGCTTAATCATCAAACACTCAA 1021

Qy 279 GluThrLeuIleProAspCysGlnLysLysPheAspSerIleMetAspMetLeuGln 298
 Db 971 GAT----- 1081

Qy 299 ArgGlnGlyLeuArgProIleProGluAlaGluIle-----GlyLeuAlaValIlePhe 316
 Db 1022 CAAGGAGATAAAAGAAGATGCCAAAGTAAGGTTCGTCAGACTGTTAAACCTCTT 1082

Qy 317 MetThrThrLysAspThrCysAspPro-----GlnGlyHisPheSerThrGlyLeuLys 334
 Db 1082 AGTTCACCTAAAGCTGGTCCTGGATCAGAAATTCTGAGGCT-----GTGAAG 1122

Qy 335 ThrThrThrProGlyProSerLeuSerGlnGlyValSerValArgGluLeuMetPro 354
 Db 1130 AAAGGAAAGCTAGTAGTGGAGAAATTACTCG-----AAAGTTGATGAACTCTAT 1177

Qy 355 SerAlaProValAsnThrThrThrThrValAlaAspThrGluSerGluGlnAlaAspThr 374
 Db 1178 -----GCTAAATAGCCCTCAAGACCTTGCTCAAAATCTCTGAAGACTATAAG 1222

Qy 375 TrpAlaLeuSerGluArgPheLysValIleLysValIleLysValIleLysValIleLys 392
 Db 1229 GCAACTACCATGAAAGCAAGTTACACAGTTAAATCAATTCTTGTAAACGCTCAAAG 1288

Qy 393 -----PheArgMetLeuUser 397
 Db 1289 CTCAGAGAAATACACCTCTTATCAAAGAACGAGTGAATAATTGATAGGTATGAGT 1348

Qy 398 GlnAspAlaProThrValLysThrSerSerAsnAsnSer-----Ser 415
 Db 1349 GAGACCTTGAGGACAGGTGAGAAAGCAATTAACTTCATGGAAGGCTTAATTAGAGAT 1405

Qy 416 MetValSerAsnThrLeuAlaLysMetArgIleProAspLysGlnLeuSerProThrLys 435
 Db 1409 TTGGTTGCGAAATCTAAAGAAATCTGAGAATTCGAGAAACACTTAATCAATTCTCAA 1466

Qy 436 ---LeuProSerIleAsnLysSerLysAspArgAlaSerIle-----GlnGlnGlnThr 452
 Db 1469 AATCTTCCAGAAATTAAGCAACTAGAAGGTCATGAAACTGAAAGCTTCATA 1525

Qy 453 AsnSerIleArgAsnThrPhe-----GlnProSerThrLysLysArg-----Glu 467
 Db 1529 GAGGATTTTAGAAAAAATTTAAAAGCTGAGAGCAAGTGCACCAAAACGCTCAA 1568

Qy 468 ArgAspP-----GluGluAsnGlnGluIleSerSerCysLysSerAlaArgIle 483

1589 CGAGATTAGCTGCTAATGAAATAATCACAA-----AAGATT 1627
 Qy 484 GluThrSerCysSerLeuLeuGluLnhGlnProAlaThrProSerLeuTrpLysAsn 503
 Db 1628 GAGTTAACAGTTCA-----CCAGAACATACTACTATATGAAAGT 1669
 Qy 504 LysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPhe 523
 Db 1670 GAAGACTGTTGAAATTCA-----GTCAAGCTAAACTGATCTGAAAGCAGC 1717
 Qy 524 ThrAsp--ThrAspLeuLysSerIleValLeuLysSerIleSerHisAlaAla 542
 Db 1718 TTGGACTCTTCACTGATCTT-----TTAACAAAATAATCCGTTGTATCA----- 1762
 Qy 543 GluLysLeuArgSerAsnLysLysArgGluMetAspAspValAlaIleLeuAspGluVal 562
 Db 1763 GATAGAATTGTCACAATTATAAGACTAAACGGATAAACATAGATGTCGCCGAATCTCT 1822
 Qy 563 LeuGluGlnLeu-----PhenylAspThrLys 571
 Db 1823 ATCAGAAATTGAAAGCTTAATGAAAGTCAACAGTGACTCTAAAGCTAAAGTATT 1882
 Qy 572 -----ProGluLeuGluIleAspValLeuValGlySerGluGluAspValAsn 588
 Db 1883 CGCAATGTAATGAAAAAACATTCACTATACAGTCGCAAAAGAACGAGAAA---CRA 1939
 Qy 589 ValArgLysArgProArgMetAspIleGluThrAsnAspThrPhsAspGluAlaVal 608
 Db 1940 GTTCTTAACACCCA-----GAGCAGAAAGTCTCTAACACGGAGAAAGGT 1987
 Qy 609 ProGluSerSerLysIleSerGlnGluAspGluLe-----GlyLysLys 623
 Db 1988 CCTCAAGAACCAAAATCAATGACAGAACAAATACAGATGATTAAATCAGCTCA 2047
 Qy 624 ArgGluLeuLys----- 627
 Db 2048 CAAGAACTGAAAAGCTTAGAAAAAGCAATAAAAGGATTAAATGGACCAACCAAGAGATCCCA 2107
 Qy 628 -----GluAspSerLeuTrp---SerAlaLysGlu----- 636
 Db 2108 TCCAAATCCAGTAGTGTATTCAAATAATTTATGGGTCTCACAAAAGGCCTATCCMG 2167
 Qy 637 -----IleSerAsnAsnAspIleGluGlnAspAspSer----- 647
 Db 2168 GAAGCCATAAAGATTTAACAGATTGAAAGTATTGGTATTCTTCAAAATACTACAGAG 2227
 Qy 648 ----- 648
 Db 2228 CACTATTAAACAAATAATATACTGATTATTGAAATTATGAACTCTCATGCCAAATGGGG 2287
 Qy 649 MetLeuProIleLysLeuLeu-----ThrGluPheAsn 660
 Db 2288 ATGGCTACTAGAAAAGTGGTTCAGTATGAAACAATAATCTGATAATGCAAAATTAAA 2347
 Qy 661 SerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly 680
 Db 2348 AAG---ATATTGAGTCAGATGAGAAGGAAAGCAGAAA-----GAAGATAATTACGGA 2395
 Qy 681 GlnLeuLysAsn-----PhenylLysPhe----- 688
 Db 2396 AGTTTAAATGATGCTTGAAGGCTATTGAAATAATTGCAAAATATTACCCATTAT 2455
 Qy 689 -----LysLysValThrThrProGlyAlaGlyLys 698
 Db 2456 AAAATTAGCAGATGTTGATGTTGGATAAAAGTACAACAAAGATCAGCCAGCACCA 2515
 Qy 699 LeuProIleIleIleGlySerAspLeuIleAlaHisAlaArgLysAsnThrGlu 718
 Db 2516 ATTCCGGA-----AATTCAAGTAATGATCAGCTTGAAGGAAAGGTAAATTGCT 2566
 Qy 719 LeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHis-----AlaLysGlu 736
 Db 2567 GTATCGAAGTATGACTAAAGTTAGTCAGTCTGCAACATCTGCCAGAAATAAT 2626

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Result No.	Score	Query	Match	Length	DB ID	Description
C 1	552.2	12.5	646	9	US-09-922-217-343	Sequence 343, App
C 2	552.2	12.5	646	10	US-09-833-263-343	Sequence 343, App
C 3	552.2	12.5	646	14	US-10-025-380-343	Sequence 343, App
C 4	537.4	12.2	541	10	US-09-878-178-1737	Sequence 1737, App
C 5	537.4	12.2	541	14	US-10-046-035-1737	Sequence 1737, App
C 6	537.4	12.2	541	15	US-10-146-02-1737	Sequence 1737, App
C 7	507	11.5	587	15	US-10-102-524-332	Sequence 532, App
C 8	405.6	9.2	468	11	US-09-918-595-13834	Sequence 13834, A
C 9	288.4	5.9	360	10	US-09-783-590-3449	Sequence 3449, Ap
C 10	239.4	5.4	272	9	US-09-923-876-5167	Sequence 5167, Ap
C 11	239.4	5.4	272	12	US-09-923-876-5167	Sequence 5167, Ap
C 12	212.6	4.8	475	10	US-09-917-800A-803	Sequence 803, App
C 13	191	4.3	404	10	US-09-783-590-8929	Sequence 8929, Ap
C 14	167.6	3.8	315	10	US-09-960-552-8727	Sequence 8727, Ap
C 15	119.4	2.7	442	9	US-09-864-761-11287	Sequence 11287, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
C 1	552.2	12.5	646	9	US-09-922-217-343	Sequence 343, App
C 2	552.2	12.5	646	10	US-09-833-263-343	Sequence 343, App
C 3	552.2	12.5	646	14	US-10-025-380-343	Sequence 343, App
C 4	537.4	12.2	541	10	US-09-878-178-1737	Sequence 1737, App
C 5	537.4	12.2	541	14	US-10-046-035-1737	Sequence 1737, App
C 6	537.4	12.2	541	15	US-10-146-02-1737	Sequence 1737, App
C 7	507	11.5	587	15	US-10-102-524-332	Sequence 532, App
C 8	405.6	9.2	468	11	US-09-918-595-13834	Sequence 13834, A
C 9	288.4	5.9	360	10	US-09-783-590-3449	Sequence 3449, Ap
C 10	239.4	5.4	272	9	US-09-923-876-5167	Sequence 5167, Ap
C 11	239.4	5.4	272	12	US-09-923-876-5167	Sequence 5167, Ap
C 12	212.6	4.8	475	10	US-09-917-800A-803	Sequence 803, App
C 13	191	4.3	404	10	US-09-783-590-8929	Sequence 8929, Ap
C 14	167.6	3.8	315	10	US-09-960-552-8727	Sequence 8727, Ap
C 15	119.4	2.7	442	9	US-09-864-761-11287	Sequence 11287, A

ALIGNMENTS

RESULT 1	US-09-922-217-343/C	SEQUENCE 343, Application US/09922217
		; GENERAL INFORMATION:
		; APP LICANT: Xu, Jiangchun
		; APP LICANT: Lodds, Michael J.
		; APP LICANT: Sechrist, Heather
		; APP LICANT: Benson, Darin R.
		; APP LICANT: Meigher, Madeleine Joy
		; APP LICANT: Stolk, John A.
		; APP LICANT: Wang, Tongtong
		; APP LICANT: Jiang, Yuqiu
		; APP LICANT: Smith, Carole Lynn
		; APP LICANT: King, Gordon B.
		; APP LICANT: Wang, Ajun
		; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
		; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
		; CURRENT APPLICATION NUMBER: US/09/922,217
		; CURRENT FILING DATE: 2001-08-03
		; NUMBER OF SEQ ID NOS: 1124
		; SOFTWARE: FastSEQ for Windows Version 4.0
		; SEQ ID NO: 343
		; LENGTH: 646
		; TYPE: DNA
		; ORGANISM: Homo sapiens
		; US-09-922-217-343
		Query Match Similarity 12.5%; Score 552.2; DB 9; Length 646;
		Best Local Similarity 93.0%; Pred. No. 2.6e-110; 4; Mismatches 32; Index 10; Gaps 3;
		Matches 609; Conservative 32; Index 10; Gaps 10;
Qy	3419 AAAACCTTCAGCTTCTAGGAACAGAAATTGGTAGCCAAATCTGCAATTCTACT 3478	
Db	645 AAAGCTTCAGCTTCTAGGAACAGAAATTGGAGCCAAATCTGCAATTCTACT 586	

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QY 3479 ACAGGATGAGGACCGATTGAGATTATGAGAATTATGAGACTTAAATT 3538
 Db 585 ACAGCCATGAGACCACTTAAATT 526
 Db 585 ACAGGGATGAGGACCGATTGAGATTATGAGACTTAAATT 526
 QY 3539 ATGATAGTGTGATGACATGGGACTTTAGAAGTGAATTGACAGGCC 3598
 Db 525 ATGATAGTGTGATGACATGGGACTTTAGAAGTGAATTGACAGGCC 466
 Db 525 ATGATAGTGTGATGACATGGGACTTTAGAAGTGAATTGACAGGCC 466
 QY 3599 ATATTAGTGTGATGAAATGGGACTTTAGGATCTTAAATTAATACCA 3658
 Db 465 ATATTAGTGTGATGAAATGGGACTTTAGGATCTTAAATTAATACCA 406
 Db 465 ATATTAGTGTGATGAAATGGGACTTTAGGATCTTAAATTAATACCA 406
 QY 3599 ATATTAGTGTGATGAAATGGGACTTTAGGATCTTAAATTAATACCA 3658
 Db 405 ATGTGAAGCTGTGGAAACATGGCTCCATTAAAGTAAAGGATTTAGGAGATT 346
 Db 405 ATGTGAAGCTGTGGAAACATGGCTCCATTAAAGTAAAGGATTTAGGAGATT 346
 QY 3659 AGTGAAGCTGTGGAAACATGGCTCCATTAAAGTAAAGGATTTAGGAGATT 3718
 Db 3659 AGTGAAGCTGTGGAAACATGGCTCCATTAAAGTAAAGGATTTAGGAGATT 3718
 QY 3719 AATATTGTYYCTGTCAATGCCCAATCCCTTAAGAAGACTGCCCTACTATAGCAG 3778
 Db 345 AATATTGTYYCTGTCAATGCCCAATCCCTTAAGAAGACTGCCCTACTATAGCAG 286
 Db 345 AATATTGTYYCTGTCAATGCCCAATCCCTTAAGAAGACTGCCCTACTATAGCAG 286
 QY 3779 TTTTTATATTGTCAATTATGATAATGAAATGAGGAGTTCTGGTCTT 3838
 Db 285 TTTTTATATTGTCAATTATGATAATGAAATGAGGAGTTCTGGTCTT 227
 QY 3839 ACAATAATTGGGTTGTCCAGPATTTCCCTTTAACCMTCICAATTGGGTCT 3898
 Db 226 ACAATAATTGGGTTGTCCAGPATTTCCCTTTAACCMTCICAATTGGGTCT 171
 QY 3899 AGGTGGATGTTCCATTGGTTTAATTGTGATAATGGGTCT 3958
 Db 170 TGATG-----TTTCAATTGGGTCTTGGTTTAATTGTGATAATGGGTCT 116
 QY 3959 AGAAATTCTTTATACATTCTAGATGCAAGGCTCTGTCGGGATAACGGATATA 4018
 Db 115 AGAAATTCTTTATACATTCTAGATGCAAGGCTCTGTCGGGATAACGGATATA 56
 QY 4019 CACCTAGTGTGGCTTGACTGTCTTGTGAAATTAGAAGTTT 4073
 Db 55 CACCTAGTGTGGCTTGACTGTCTTGTGAAATTAGAAGTTT 1
 RESULT 3
 US-10-025-380-343/c
 ; Sequence 343, Application US/10025380
 ; Publication No. US20020182191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Sechrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Clipper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vediwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121-471C12
 ; CURRENT APPLICATION NUMBER: US/09/833,263
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 1033
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 343
 ; LENGTH: 646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-83-26-343
 RESULT 2
 US-09-83-26-343/c
 ; Sequence 343, Application US/09833263
 ; Patent No. US2002011547A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121-471C12
 ; CURRENT APPLICATION NUMBER: US/09/833,263
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 1033
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 343
 ; LENGTH: 646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-025-380-343
 RESULT 1
 US-09-83-26-343
 ; Sequence 343, Application US/09833263
 ; Patent No. US2002011547A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vediwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; OF COLON CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121-471C14
 ; CURRENT APPLICATION NUMBER: US/10/025,380
 ; NUMBER OF SEQ ID NOS: 1129
 ; SEQ ID NO: 343
 ; LENGTH: 646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-025-380-343

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181 ATATTAGTGTATGAAATGGAGTCATTGGAGTCATTGTAGTCCTAAAGCCATGTATCATAATTACCA 240
 QY 3659 AGTGAAGCTGGAGACATATGGTCATTCATTAGTAAAGGATATAATGGACAGATT 3718
 Db 241 AGTGAAGCTGGAGACATATGGTCATTCATTAGTAAAGGATATAATGGACAGATT 300
 QY 3719 AATATTGTTTCTGTCATGCCAACATCCCTTCATAAGGAGACTGCCCTACTATAGCG 3778
 Db 301 AATATTGTCCTGTCATGCCAACATCCCTTCATAAGGAGACTGCCCTACTATAGCG 360
 QY 3779 TTTTTATTTGTCAATTATGATAATAATGAAATGAGGAGTTCTGTACTCTGTCCT 3838
 Db 361 TTTTTATTTGTCAATTATGATAATAATGAAATGAGGAGTTCTGTCCT 419
 QY 3839 ACAATAATGGGTGTTCCAGTATTTCACMTCCACATTGGTGTGT 3898
 Db 420 ACAATAATGG---TGTGTCAGATTTCCTTTAACATCCACATTGGTGTGT 475
 QY 3899 AGGTGATGTTCCATTGGTTTAATTGTATPATCCCTGATGCTATAATTGGTCAT 3958
 Db 476 TGATG---TTTCAATTGGTTTAATTGTATPATCCCTGATGCTATAATTGGTCAT 530
 QY 3959 AGAAATTCTTATACATTCTAGATGCAAGSTCTCTGTGCGGATAACGTTGAGATA 4015
 Db 531 AGAAATTCTTATACATTCTAGATGCAAGSTCTCTGTGCGGATAACGTTGAGATA 587

RESULT 8
 US-09-918-995-13834
 ; Sequence 13834, Application US/0918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYSED, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEAR ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 13834
 ; LENGTH: 468
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) .. (468)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-13834
 Query Match 9.2%; Score 405.6; DB 11; Length 468;
 Best Local Similarity 97.4%; Pred. No. 2.3e-78;
 Matches 411; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Db 2938 TGGCTTACTGAGCTGGGGGGCTGCTGTTGAGCTTATTTAGTCAGTTTCTCA 2997
 QY 47 AACATGAATGTCATTGAGCTGGGGGGCTGCTGTTGAGCTTATTTAGTCAGTTTCTCA 106
 Db 2998 CTTATAAAGTAAATGAAATGTCAGATGTTCTTCTACCKTAAGGGAGATGGTAA 3057
 QY 107 CTTATAAAGCAGAACG3GAGATGGTGTGTTCTACCTTAAGGGAGATGGCAGA 166
 Db 3058 AACATGAATGTCATTGAAACTTATGACAGTGTGTTGAGCTTATTTAGTCAGTTTCTCA 3117
 QY 167 AACATGAATGTCATTGAGCTGGGGGGCTGCTGTTGAGCTTATTTAGTCAGTTTCTCA 226
 Db 3118 ATATATTCAATGACTCTGATCCAGCAAAGGGAGTTCAAGACTCAACT 3177
 Db 227 ATATATTCAATGACTCTGATCCAGCAAAGGGAGTTCAAGACTCAACT 286
 QY 3178 GATTAGTGTATGAAATGAGAATGGAAATGGAAATGGAAATGGAAATGGCACTTCCATCA 3237

RESULT 9
 US-09-783-590-3449
 ; Sequence 3449, Application US/09783590
 ; Patent No. US2002010850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Patrick J.
 ; APPLICANT: Haeultine, William A.
 ; APPLICANT: Li, Haodong
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 ; FILE REFERENCE: PO-16-2C1
 ; CURRENT APPLICATION NUMBER: US/09/783,590
 ; CURRENT FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 08/420,856
 ; PRIOR FILING DATE: 1995-04-12
 ; PRIOR APPLICATION NUMBER: 08/346,731
 ; PRIOR FILING DATE: 1994-11-21
 ; NUMBER OF SEQ ID NOS: 12485
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3449
 ; LENGTH: 360
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (115)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (164)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (251)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (310)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (320)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (327)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (328)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (329)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (359)
 ; OTHER INFORMATION: n equals a,t,g, or c

US-09-783-590-3449

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APPLICANT: Johnson, Koty
 APPLICANT: Castle, Arthur
 APPLICANT: Blashoff, Michael
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917,800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,880
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/290,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/290,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/292,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 803
 LENGTH: 475
 /
 / TYPE: DNA
 / ORGANISM: Rattus norvegicus
 /
 / FEATURE:
 / OTHER INFORMATION: Genbank Accession No. US200202101
 /
 / US-09-917-800A-803
 /
 Query Match 4.8%; Score 212,6; DB 10
 Best Local Similarity 73.5%; Pred. No. 3,5e-36;
 Matches 336; Conservative 0; Mismatches 94;
 /
 Qy 1996 GATGCTTCAAAAAGGCTCTTATGACTGATTAGATC
 Dbs 460 GAGGCTTCAAGAAAATCTGCTGACTGATTAGGTCA
 Qy 2056 TTCCAGAAATCCCTGGATAAATGATGATTATGGTCA
 Dbs 400 TTCCAGAAATCTGGCCCACTAA -- ATGGTCGTTGGTGA
 Qy 2116 CAAAAAGGTCACTATCCCTGGACCGGAAACCTCCACAA
 Dbs 343 CAGAAGGCTACGTCCGACGGAAAGCTTCCACAA
 Qy 2176 AATAGCTCATCATGCTCGAAGATACTGAGACTAGAGAC
 Dbs 283 ATAGGGTCACATGCTCGAAGATACTGAGACTAGAGAC
 Qy 2236 GGTACACAAATCAACATGCAAAAGAGAGTCTTGTGTA
 Dbs 223 GGTACAGAAACAAAGGCAAAAGGACTCTTGTGTA
 Qy 2296 TTATTTAAAAGGAGAAAGATAACTGAGGATTAAAGAG
 Dbs 163 TAATGTAATA -- AGAAGATAATGAACTTAAAGAA
 Qy 2356 GTAAGGATCTACTTCAGGCCAACAGGTATATGATATA
 Dbs 110 -----TCTACTTCAGACAACTGGGATCTGGTAAATGATGTT
 Qy 2416 AGTACAAATGTTTATGGCTAAATTATTAATAAA 24
 Dbs 67 ATTACAAATGTTAAGGCTTCAGTTTAAATTAATAAA 3

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Qy 3367 TGCAGGTTGAAAC-TCCAACTGGCAAGGG -AGTTAGGGAAATGAAGGTTTTTTT--AA 3420
 Db 248 TGGCAAGTGGACTTCAGCTGAAGGGAAATGAAGGTTTTTTAA 307
 Qy 3421 AAGCTTCAGCTTCCCTAGGG 3442
 Db 308 AAGCTTCAGCTTCCCTAGG 329

RESULT 14 /
 US-09-860-352-8727
 ; Sequence 8727, Application US/09960352
 ; Patent No. US20020127139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; SEQ ID NO: 15112
 ; LENGTH: 315
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 37-LIB34-077-Q1-B1-B10
 US-09-860-352-8727

Query Match 3.8%; Score 167.6; DB 10; Length 315;
 Best Local Similarity 76.3%; Pred. No. 1.9e-26;
 Matches 206; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 897 TCCCTGACTGTGAGAAATGGATTCAGTCATAATGGATATGCTCAAAGCCAGGTC 956
 Db 15 TTAAGGACTCACAGATGAGGCATONTCAACTGCTATACTCCAGGGGGTC 74

Qy 957 TTAGACCTATTCTGAAAGCAGAAATTGGATTGGCGGTGATTTCATGACTAACAGAAATT 1016
 Db 75 ATAGAGCTTTCAGAGCAGAAATTGGCTAACGTTCAATTGTTACAGAAACT 134
 Qy 1017 ACTGTGATCTTCAGGGCATCCAGTACAGGATTAAAGACAACCTCCAGGACAAGCC 1076
 Db 135 ACTGTGATACATAGGGGACGCGATACAGGATTGAGAAACACTCCAGGTCAAAC 194
 Qy 1077 TTTCACAAAGGGGTCAAGTCATGATGAAACTAAATGCCAAGGCCCACTGAACTACA 1136
 Db 195 TTTCACAAAGCCCTAACACCCATGAGAATTCATGCCAATGCCCTACAGAACGACA 254

Qy 1137 CATACTGATGTCACAGAACTCAGCAAG 1166
 Db 255 CATACTGATGTCACAGAACTCAGAACATG 284

RESULT 15
 US-09-864-761-11287
 ; Sequence 11287, Application US/09864761
 ; Patent No. US2002004873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04